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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 23, 2002, 16:34:22; Search time 69.24 Seconds (without alignments) 1084.341 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-816-011F-63
2294
1 MVIINRSNTYAVEQEAFPRD......LTGGLWPVVIEHFVDKPSIL 434

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_vertebrate:*
sp_unclassified:*
sp_uvrius:*
sp_bacteriap:*
sp_archeap:* sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:* sp_plant: *
sp_rodent: *
sp_virus: * SPTREMBL_19:* |: sp_archea:# | sp_bacter1a Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Res

Description	019495 caenorhabdí	09u318 caenorhabdi			_	021145 caenorhabdi	099065 musculu	Oguiv2 homo sapien	O9bq85 orvetolagus	09jit8 mus musculu	O9bzd2 homo sapien	O9m5x9 arabidopsis	064603 arabidopsis			Q9jiml mus musculu
ID	019495	Q9U3L8	023599	093871	Q9VMB6	021145	099P65	09UJY2	Q9BG85	Q9JIT8	Q9BZD2	O9M5X9	064603	Q9DBT8	Q9JHF0	Q9JIM1
DB	2	വ	ഗ	ഗ	Ŋ	Ŋ	11	4	ဖ	Η	4	10	10	11	11	11
Query Match Length DB	434	418	461	450	458	800	475	456	456	456	475	428	428	458	458	460
Query Match	98.7	35.0	31.2	30.8	28.1	25.0	16.0	15.0	14.7	14.3	14.3	14.0	13.7	13.2	13.2	13.1
Score	2265	802	716.5	706.5	645	574.5	367.5	343.5	336.5	328.5	327.5	320.5	313.5	302.5	302.5	301.5
esult No.	-	7	ιú	4	S	9	7	8	σ	10	11	12	13	14	12	16

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Q99K84 Q9NK81 Q9SKN3 Q9SKN3 Q9FWY1 Q9VPQ0 Q9VPQ0 Q9GTP5 Q9GG84 Q93G90 Q96EB2 Q96EB2 Q96EB2 Q96EB2 Q96EB2 Q96EB2 Q96EB2 Q96EB2 Q96EB2 Q90EB4 Q9NBV4 Q9	Q944N9 Q9M0Y2 Q9Y0I0
11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	10
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	418 463
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301.5 291.5 291.5 261.5 221.5 217.5 217.5 195.5 195.5 182.5 181 181 181 181 181 181 181 181 181 18	138.5 136
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ALIGNMENTS

62 8 242

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TGVVTGXPTVXSSNFQSFQTIASQVPNLLLNIFILVVKGGLASRI--TVGLSIVAVCV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida, Rhabditoidea;
Rhabditidae, Peloderinae; Caenorhabditis.
IINRSNTYAVEQEAFPRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVE
              TWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILLVIVL
                                                                            | | : | :: :|| | : | THANDSFQSAMGVVAQVPNLIVAIINVLNLIRGPLLYRVLAPLAFNSLLIVIILALVIFQ
                                                                                                                         EPTEDSMSWFFWVTLGMATSINFSNGL/Y ENSVYGVGGDFPHTY IGALLIGNNICGLLITV
                                                                                                                                       DRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYT
                                                                                                                                                                                                                                                                                                                303 LLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFF
                                                                                                                                                                                                                                                                                                                              290 GIAVFLNFNFFAAVGNVAATFVTFPGPRLLIVPCVIRLEIPFFMFSNYLPHSRTMGVLF
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                                                                                                                                                                                                                                                                                                                                                                                             350 TNEWIFFFGUTLLAFTSGYFSSLGMMYTPRVCPPEYSKLAGQVSALSLVLGITAG
                                                                                                                                                                                                                                                                                                                                                                            363 ESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dobson R.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 282:zviz ...
EMBL: 268303; CAA92642.1; -.
EMBL: 268303; CAA92642.1; -.
Pfam; PF01733; Nucleoside_tran; 1.
Pr00703; Nucleoside_tran; 1.
Pr005003; PD05103; DER_Nucleoside_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                     31.2%; Score 716.5; DB 5; 35.8%; Pred. No. 1e-50; ive 86; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM
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                                                                                                                                                                                                    VLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLI 180
                                                                                                                                                                                                                      TVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEIREKA 240
                                                                                                                                                                                                                                                                                                                                                                                              YTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPV 360
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                                             Gaps
                                                                                           Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_FaxID=6239;
                                                                                                                                                                                                                                                                                                                                                MVIINRSNTYAVEQEAFPRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDG
                                                                                                                                                                                                                                                                                                                                ETDRPSPSILWITFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEI
                                            0;
             Length 434;
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Pred. No. 9.5e-58;
; Mismatches 135; Indels
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
InterPro: IPR002259; DER_Nucleoside_tran.
Priam; PF01733; Nucleoside_tran; 1.
ProDom; PP01513; DER_Nucleoside_tran; 2.
SEQUENCE 418 AA; 46333 WW; 5CBDD27EE06BFC8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                             4
              DB 5;
             Score 2265; DB 5;
Pred. No. 2e-177;
); Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode
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37.6%;
             98.78;
99.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.0
Best Local Similarity 37.6
Matches 156; Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                           Similarity
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                Query Match
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                                Local
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                               Best Loc
Matches
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Gaps

39;

Indels

5

Gaps

40;

84;

Length 461;

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RA MEDLINE=20190005; PubMed=1073132;
RA MEDLINE=20190005; PubMed=1073132;
RA Amanatides P.G., Scherer S.E., Itoht R.A., Bonskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortman J.R., Zhangell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortman J.R., Tanderwale, C.R., Miklos G.L.G.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Mayarer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxendale J., Bayaraktaroglu L., Basaley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Horbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferrac S., Plasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Classer K.,
Glodek A., Gong F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kallush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kallush F., Karpen G.H., Well M.-H., Indeywam C.,
Alalali M., Murphy B., Murphy L., Muzny D.M., Nelben D.L.,
Rount S.M., Moy M., Murphy B., Murphy L., Muzskern D.R., Palacel D.M.,
Raber D.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Ruber E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Ruber E., Spradling D.M., Weinstock G.M., Weissenbach J.,
Raber B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith H.O.,
Raber S. T., Reder T., Woodage T., Wolter E., Wang G., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao G., Zha
     :|:: : || : | | : || |:| |: || VILLSMSTKAVTRNILDR----SFAYFSIALITLVFCFISFHILKKQRFYQFYSTRAERQ 254
                                                                                                                                                                                                                    353 VQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMV 412
                                                                                                                                                                                                                                                                                                                             373 PETRTLEVFFESTWLFIIVAASMSFGSGYFSGLSMMYTSKTVDPSKAQVAGWAAGFFLIS 432
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                     R---EKAETDRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFP-VMMTVTTRGDSGFLNK
                                                                                                                                    RAKNEEAADNEGKMANYIATEKEAFPOLINVFLVFFVTLSIFPGVMMYVKDEKKGGTYDF
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Last annotation update)
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BEST:LD04971 OR CG11045.
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433 GIVSGLIFTMVIKFVV 448
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NCBI_TaxID=7227
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                                         ITTMMFIYVETSTWLTGFFTLTITITIVLNGANGVYQNSIFGLASELPFKYTNAVIIGNN 188
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                                                                                                                                                                                                              KGMEIREK---AETDRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFP-VMMTVTTRGDS 287
                                                                                                                                                                                                                                                                                                                  G-----FLNKIMSENDEI----YTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLK 333
                                                                                                                                                                                                                                                                                                                                                   334 FAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 ITVVKI --- GVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                    ICGLLITVVKI --- GVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Swinburne J.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002259; DER_Nucleoside_tran.
Pfam; PF01733; Nucleoside_tran; 1.
ProDom; PD005103; DER_Nucleoside_tran; 1.
SEQUENCE 450 AA; 50495 MW; CF3973D5EE517909 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 VPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | :: | :: | : | 425 VDPSKAQVAGMMAGFFLISGIVSGLIFTMVIKMVV 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z79601; CAB01882.1; -.
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01-FEB-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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nes 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Gaps

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Length 800;

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QLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSWFFWVTL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 VAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEIREKAETDRPSPSILWTT---- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 FINCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 AAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQ--TRAYPVFFESTDIFVIG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydra R.J., Cass C.E., Young J.D., Baldwin S.A.;
"The ENT family of eukaryote nucleoside and nucleobase transporters: recent advances in the investigation of structure/function relationships and the identification of novel isoforms.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF326986; AAK00957.1; ...
Interpro; IPR002259; DER_Nucleoside_tran.
Pfam. PF01733; Nucleoside_tran; 1.
PRINTS; PR01130; DERENTWSPRT.
Probom; PD005103; DERENTWSPRT.
                                                                                                                                                                                                                                                                                                                                     19 RDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFK-PDGVETWYSKEFMGSLTIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 ICIFALTSGYLSSLIMMYAPR---SHEDPKIQRMAGMIASFFLIFGIVAG 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 GIAMSFSHGYLSALAMGYTPNVVPSH----YSRFAAQLSVCTLMVGLLTG 417
                                                            C.elegans: A platform
                                                                                                                                                                              DER_Nucleoside_tran; 1.
; 90383 MW; E056D51129E4BF45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EQUILIBRATUE UNCLEOSIDE TRANSPORTER 3.
                                                                                                                                                                                                                                                       25.0%; Score 574.5; DB 5; 32.7%; Pred. No. 7.8e-39; ive 88; Mismatches 165;
                                                                                                                 EMBL; Z77665; CAB01223.1; -. InterPro; IPR002259; DER,Nucleoside_tran. Pfan. PF01733; Nucleoside_tran; 1. Probon; PP005103; DER_Nucleoside_tran; 1.
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SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                        "Genome sequence of the nematode
investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                             Matches 134; Conservative
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099P65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 IGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSW--- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 FASQIPNLVFNWLNIFVNFGGDLTTRIVYSIIFEMVILLVTIILAML-----DSSQWPGV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                           STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Conzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003614; AAF52405.1;
EMBL; AV05847; AAL135761;
FIYBase; FB970026585; BEST:LD04971.
InterPro; IRR0022639; DER_NUCLeoside_tran.
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McMurray A.A.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                               PRINTS; PR01130; DERENTRNSPRT.
ProDom; PD005103; DER_Nucleoside_tran; 1.
SEOUENCE 458 AA; 51324 MW; 72D36D64CE0D4A2E CRC64;
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Last annotation update)
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%; Score 645; DB 5; 32.9%; Pred. No. 7.4e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 138; Conservative
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                                                                              SEQUENCE FROM N.A
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Q21145;
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EMBL; BC001382; AAH01382.1;
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                                                                                                                     112;
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
601-DEC-2001 (TrEMBLRel. 19, Last annotation update)
601LIBRATIVE NUCLEOSIDE TRANSPORTER 1 (SOLUTE CARRIER FAMILY 29
(NUCLEOSIDE TRANSPORTERS), MEMBER 1) (SIMILAR TO SOLUTE CARRIER FAMILY
29 (NUCLEOSIDE TRANSPORTERS), MEMBER 1).
                                                                                                                                                                        NYWFKPDGVETWYSKE-----FMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVF 102
                                                                                                                              103 APVCFNIVNLTIILILVIVLEPTEDSMSW---FFWVTLGMATSINFSNGLYENSVYGVGG 159
                                                                                                                                                                                                                                                                                                                                    315 AIGSIVASKIHWPTPR--YLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIF-VIG 371
                                                      Gaps
                                                                          -----PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                    'Genomic Seugence of the human Equilibrative Nucleoside Transporter
                                                                                                                                                                                                                                                                                                                                                                                         DFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFF
                                                                                                                                                                                                                                                                                                                                                                            372 GIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                        SFPMRNAQALISGGAMGG-TVSAVALLVDLAASSDVRDSTLAFFLAMAAVFLGLCMGLYLL
                                                                                                                                                                                                                                               220 ITKQDFYHYHHQKGMEIREKAETDRPS---PS-------ILWTTFTNCY
                                                                                                                                                                                                                                                                    251 LSQLEYARYYMRPVAPVRVFSGEDNPSQDAPSASSVAPASRVMHTPPLGPILKKT----
                                                                                                                                                                                                                                                                                         259 GOLFNVWFC----FAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                     77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Graham K.A., Coe I.R., Carpenter P., Baldwin S.A., Young J.D.,
                                 Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF190884; AAF02777.1; -.
 F593D5D03C6CBB52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                 DB 11;
                               ; Score 367.5; DB 11;
; Pred. No. 3.9e-22;
83; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-MUSCLE, RHABDOMYOSARCOMA;
 51719 MW;
                                16.0%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-COLON ADENOCARCINOMA;
                                Query Match
Best Local Similarity 25.8
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                        SNTYAVEQEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
 475
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFASVAMI-CAIASGSELSESAFGYFITACAVIILTIICYLGLPRLEFYRYYQQLKLEGP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 GEQETKLDLISKGEEPRAGKEESGVSVSNSQPTNESHSIKAILKNISVLAFSVCFIFTIT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWP--TP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICG 1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYLKFAIILRALFIPFFFFCNYRVQTRAY-PVFFESTDIFVIGGIAMSFSHGYLSALAMG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|:| |: :::| ||||||| |:| |:| || PQDRYKAVWLIFFMLGLGTLLPWNFFMT-ATQYFTNRLDMSQNVSLVTAELSKDAQASAA 65
                                                                                                                                                                                                                                                                                                                                                                                                       PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVE---TWYSKEFMGSLT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PVCFNIVN----LTIILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KGMEIREKAETDRPSPSILWTT-----FTNCYGQLFNVWFCFAVT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 LLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQ-----
                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                        Length 456;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleoside transport.";

subfiltad (NOV-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF323951; AAK11605.1; ...

InterPro; IPR002259; DER_Nucleoside_tran.

Pfam; PF01733; Nucleoside_tran; 1.

PRINTS; PR01130; DERENTRNSPRT.

ProDom; P0005103; DER_Nucleoside_tran; 1.

PRODOM; P0005103; DER_Nucleoside_tran; 1.
EMBL; BC008954; AAH08954.1; -.
InterPro; IPR002259; DER_Nucleoside_tran.
Pfam; PF01733; Nucleoside_tran; 1.
PRINTS; PR01130; DERENTRNSPFT.
PRIODM; PD005103; DER Nucleoside_tran; 1.
SEQUENCE 456 AA; 50219 MW; F18535A95DEBC95D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
NBMPR-INSENSITIVE NUCLEOSIDE TRANSPORTER EI
                                                                                                                                                                                                                                                                    15.0%; Score 343.5; DB 4; 24.3%; Pred. No. 3.4e-20; Live 77; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | : | : | | : | | FPERKKVKPAEAETAGAIMAFFLCLGLALGAVFSFLFRAIV 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGSQLP--NASINVFNLFLIIAGPLIYRVFA-----
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2001 (TrEMBLrel. 18, Last ann
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259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AAIGSIVASKIHWP---TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| :| || : | || || : 380 DWLGRSLTSYFLWPDEDSQQLLPLLVCLRFLFVPLFMLCHVPQHAR-LPIIFRQDAYFIT 398
                                                                                                                                    TDTFNFNNWVTLLSQLPLLLFTLLNSFLYQCIPESVRILG----SLLAILLLFALTAALV 116
                                                                                                                                                                                                                                                                                                                                                                                                                            231 TQELETKAELLQADEKNGVPISPQQASPTLDLDPEKEPEPEEPQKPGKPSVFVVFRKIWL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 QLFNVWFCFAVTLTIFPVM--MTVTTRGDSG----FLNKIMSENDEIYTLLTSFLVFNLF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PDGVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYR 100
                                                                                          -----LTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILLLVIVLE 123
                                                                                                                                                                                                                                      117 KVDLSPGLFFSVTMASVWFINSFCAVLQGSLFGQLGTMPSTYSTLFLSGQGLAGIFAALA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The BNT family of eukaryote nucleoside and nucleobase transporters:

"The ENT family of eukaryote nucleoside and nucleobase transporters:
recent advances in the investigation of structure/function
relationships and the identification of novel isoforms.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AR36997; ARX00358.1;
InterPro; IPR0012259; DER_Nucleoside_tran.
PFONTYS; PR01130; DERENTRSPRT.

PRODOM: PD005103; DERENTRSPRT.

SEQUENCE 475 AA, 51874 MW; 59089BBA5C75FA2C CRC64;
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72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SNTYAVEQEAF-----PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 PTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVV
                        ----TKQDFYHYHHQKGMEIR--------EKAETDRPSPSILWTTFTNCYG
                                                                                                                                                                                                                                                                                        184 KI-----GVTYFLNDEPKLVAIVYF---GISLVILLVCAIAL-----FFI-----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEFMGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 FMLLFAVSNGYLVSLTMCLAPRQVLPHEREVAGALMTFFLALGLSCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 GGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202;
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24.4%; Pred. No. 7.3e-19;
ive 83; Mismatches 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>::</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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TISSUE=PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                 13;
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MEDLINE-20539821; PubMed=11085929;
Kiss A., Farah K., Kim J., Garriock R.J., Drysdale T.A., Hammond J.R.;
Kiss A., Farah K., Kim J., Garriock R.J., Drysdale T.A., Hammond J.R.;
"Molecular cloning and functional characterization of inhibitor-
sensitive (mENT1) and inhibitor-resistant (mENT2) equilibrative
nucleoside transporters from mouse brain.";
Biochem. J. 352:363-372(2000).
EMBL; AF183397; AAF78477.1;
                                                                                                                                                                                                                                                                                                                   259 GQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTALCEVLVFTVTLSVFPAITAMVTSSTS-----PCKWSEFFNPICCFLLFNVMDWLGR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 IVASKIHWP--TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMS 376
                                                                                                                                                                                          ----LIIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDS 128
                                                                                                                                                                                                                                                                                        MSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGL-----LITVV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIREKAE-----TDRPSPSILWTTFTNCY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELETKAELLQCDEKNGVPSSPQKAALTSDVDPEKEPELEPAEPRDPGKPSV-FVVFRKIW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLTSYFLWPVENSKLLPLLVRLRFLFVPLFMLCHVPQRAR-LPILFPQAANFIIFMLLFA 404
                                                                                                                                                                                                                                         66 FNNWVTLLSQLPLLFTLLNSFLYQCIPEAVRILG----SLLAMLLLFALTAALVKVDVS 121
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                             18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEFMGS---- 72
                                                                                                                             ||| |::| ::| ||||| ||| || || PRDSYHLVGISFFILGLGTLLPWNFFITAIP-YFQGRLAGANGTAGALSTNHTGPTDAFN 65
                                                                                                                                                                                                                                                                                                                                                                                                                184 KIGVTYFLNDEPKLVAIVYF---GISLVILLVCAIALFFITKQDFYHYHHQK-----GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%; Score 328.5; DB 11; Length 456; 24.2%; Pred. No. 5.8e-19; ive 68; Mismatches 191; Indels 95;
  Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EQUILIBRATIVE NITROBENZYLTHIOINOSINE-INSENSITIVE NUCLEOSIDE
TRANSPORTER ENT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pram: PF01733; Nucleoside tran; 1. Pram: Pr01733; Nucleoside tran; 1. PRINTS; PR01130; DERENTRNSPRT. ProDom; PD005103; DER_Nucleoside_tran; 1. SEQUENCE 456 AA; 50255 MW; A9FE7CA037A4468F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 VSNGYLVSLTMCLAPRQVLAHEREVAGALMTFFLALGLSCG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 FSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG 417
    DB 6;
                                                 68; Mismatches 195;
                        .3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
    Score 336.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1345278; S1c29a2.
InterPro; IPR002259; DER_Nucleoside_tran.
                           Pred. No. 1
  14.7%;
24.9%;
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.2
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLC29A2 OR ENT2
                                                 Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
       Query Match
                               Best Local
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11;
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STRAIN-CV. COLUMBIA,
STRAIN-CV. COLUMBIA,
Vysokaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji O.,
Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
Theologis A.,
                         242
                                                                                                                                            337
                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LVALVCLFVIVVFYAHKSLASFRINLGLLLFVIALLVVPVLDLVYVKGQVGLYAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
    |:|:::::| GSGVLVSLLRILTKAVYPQDPDGLRKSANLYFAVGIVVWVICAVFYNVAHKLPVIKFHEE
                                                                                                                                              GDSGFLNKIMSENDEIYT-LLTSF-----LVFNLFAAIGSIVASKIHWPTPRYLKFAII
                                                                                                                                                                                                                            338 LRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEFMGSLTIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | : | : | | | | | | | | | | | | 35 PSDSYHFAXIIXFTLGVGFLLPWNAFITAVD--YFSYLYPSTAVDRIFAVIXM-----
                                                               KGME--IREKAE-----TDRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTR
                                                                                                   RKNEELIREKSEEKGSLTGLAWRTTLWDIVTKVKSHGFGIVLLYMVTLSIFPGYIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLPNASINVFNLFLIIA - - - - GPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSWF
                                                                                                                                                                                    ------EDVHSELLTDWYPILLIAAYNVFDLVGKCLTAVFMLEDEKIAVGGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis thaliana chromosome 1 BAC F1707 sequence."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003671; AAC18807.1; '.
InterPro; IPR002106; AA_KRNA_ligase_II.
InterPro; IPR002559; DER_Nucleoside_tran.
Pf01733; Nucleoside_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD005103; DER_Nucleoside_tran; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SEQUENCE 428 AA; 46764 MW; B762E36C07516DB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 313.5; DB 10; 23.2%; Pred. No. 9.1e-18; tive 84; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                         428
                                                                                                                                                                                                                                                                                                           YSRFAAQLSVCTLMVGLLTGGL--WPVVI 424
                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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es 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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F1707.13.
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                                                                                                     24.3
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Matches
                       183
                                                                                                                                            285
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                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                   GVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAI 215
                                                                                                                                                                                                     216 ALFFITKQDFYHY------HHQKGMEIREKAETDRPSPSI------LWTTFTN 256
                                                                                                                                                                                                                                                                                    CYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSE--NDEIYTLLTSFLVFNLFA 314
                                                                                                                                                                                                                                                                                                                                                                    315 AIGSIVASKIHWPTP--RYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGG 372
                                                                                                                                                                                                                                                                                                                                                                                            cDNA of a putative nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------VNLTIIL-ILVIVL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FKLRNSSSPATGEDPEGSD--ILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIR 134
                                                                                                                                                                                                                                           LYLLLSRLEYARYYMRPVLAAHVFSGEE--ELPQDSLSAPSVASRFIDSHTPPLRPILKK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPTED-----SMSWFFWVTLGMATSINFSNGLYENSVYGVGDFPHTYIGALLIGNN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ICGLLITVVKIGVTYFLNDEP---KLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEFMGSLTIGS 77
                                                                                                                                                                                                                                                                                                           VFAPVCFNIVNLTIILILVIVLEP--TEDSMSW---FFWVTLGMATSINFSNGLYENSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 SLLGLSNGYLSTLALLYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 IAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%; Score 320.5; DB 10; Length 428; 22.9%; Pred. No. 2.4e-18; ive 80; Mismatches 169; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li J., Wang D.;
"Cloning and in vitro expression of the cDNA of a putati-
transporter from Arabidopsis thaliana.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF220759; AAF26446.1;
InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR002259; DER Nucleoside_tran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01733; Nucleoside_tran; 1.
PRINTS; PR01130; DERENTRNSPRT.
PRODOM; PD005103; DER_NUCleoside_tran; 1.
PROSTE; PS00339; AA_TRNA_LIGASE II_2; UNKNOWN_1.
SEQUENCE 428 AA; 46718 MW; 1433D916FAC93CB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE NUCLEOSIDE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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  80
                                                                                135
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PRELIMINARY;
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                                 DRPSPSILWTTFTUCYGQLFNVWFCFAVTLTIFPVWMTVTTRGDSGFLNKIMSENDEIYT 302
                                                                                                                                                                         GLAWRITIWDIVIKVKSHGFGIVLLYMVILSIFPGYII-------EDVHS 303
                                                                                                                                                                                                                                      -LLTSF-----LVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQT 355
                                                                                                                                                                                                                                                                                                                                                     RAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLL 415
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Nature 409:685-690(2001).
BMBL: AK004756: BAB2357.1; -.
MGD: MGI:1927073; SIC2991.
InterPro; IPR002259; DER_Nucleoside_tran.
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PRINTS; PR01130; DERENTRNSPRT.
PRODOM; PD005103; DER_NUCleoside_tran; 1.
SEQUENCE 458 AA, 50018 MW; 01F300DEBB4FA0C6 CRC64;
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Last annotation update)
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Pred. No. 7.8e-17;
2; Mismatches 215;
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MEDLINE-21085660; PubMed-11217851;
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Best Local Similarity 22.5%; Pr
Matches 104; Conservative 82;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10090;
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PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYW----FKPDGVETWYSKEFMGS 72

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STRAIN-129/SVJ1;
Chol D.-S., Messing R.O.;
"Alternative splicing variants of equilibrative nucleoside transporter
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STRAIR-CD1; TISSUE-WHOLE BRAIN;
Hammond J.R., Kiss A.J.;
"Molecular cloning of the full-length cDNAs encoding the
"nitrobenzylthioinosine-sensitive and nitrobenzylthioinosine-resistant
equilibrative nucleoside transporters from mouse brain.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EQUILIBRATIVE NITROBENZYLTHOINOSINE-SENSITIVE NUCLEOSIDE TRANSPORTER
ENTI (SOLUTE CARRIER FAMILY 29 (NUCLEOSIDE TRANSPORTERS), MEMBER
                                                                                                                                        117 ILVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNIC 176
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                  65
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LTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFN. -------IVNLTIIL
                                                                                                PTVALPARSSLSAIFNNVMTLCAMLPLLVF--TCLNSFLHQRISQSVRILGSLLAILLVF
                                                                                                                                                                LTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWP--TP
                                                                                                                                                                                                                                                                                                                                                                                                              302 IGLFP---AVTAEVESSIAG--TSPWKSYFIPVACFLNFNVFDWLGRSLTAVCMWPGQDS
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                           GLLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHQKGME-
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-OCT-2000 (TrEMBLrel. 15,
-DEC-2001 (TrEMBLrel. 19,
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TISSUE-BREAST TUMOR;
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 LIIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWP--TP 329
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                                                                                                                                                                                                                                                                                                                Query Match 13.2%; Score 302.5; DB 11; Length 458; Best Local Similarity 22.5%; Pred. No. 7.8e-17; Matches 104; Conservative 82; Mismatches 215; Indels 61;
       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131212; AAF78452.1; -
EMBL; AF21825; AAF64036.2; -
EMBL; BC006812; AA406812.1; -
MGD; MGI:1927073; S1c29a1.
InterPro; IPR002259; DER_Nucleoside_tran.
PF0173; Nucleoside_tran; 1.
PRINTS; PR01130; DER_Nucleoside_tran; 1.
PRODOM: PD005103; DER_Nucleoside_tran; 1.
SEQUENCE 458 AA; 50076 MW; EDE0FDEF5BF3E274 CRC64;
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Strausberg R.;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 23, 2002, 16:35:07; Search time 24.68 Seconds (without alignments) 680.887 Million cell updates/sec

US-08-816-011k-63 2294 1 WYIINRSNTYAVEQEAFPRD......LTGGLWPVVIEHFVDKPSIL 434 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Lesting linet 45 summaries

Database :

Pred. No. 18 the perfect of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40

	Description	Q99808 homo sapien	2 h equ		O54698 rattus norv	Q61672 m equilibra	Sa	Q58086 methanococc	P71338 haemophilus		P47344 mycoplasma	Q9et30 mus musculu	Q9hd45 homo sapien	_	$\overline{}$	P42377 lactococcus	_		P02983 staphylococ	-	_			O32086 bacillus su	P55086 mus musculu	P24884 ascaris suu	Q08485 saccharomyc	P13090 saccharomyc	P27514 saccharomyc	Q37376 acanthamoeb	Q9zym7 rhipicephal	$^{\circ}$	2485	P03910 bos taurus
SUMMARIES	OI OI	T1_H	ENT2_HUMAN	ENT2_RAT	ENT1_RAT	ENT2_MOUSE	FU26_YEAST	Y672_METJA	HITB_HAEIN	YAEC_SCHPO	Y098_MYCGE	T9S3_MOUSE	T9S3_HUMAN	NU5M_HORSE	TCR2_BACSU	YDNK_LACLC	NAPA_ENTHR	PAR2_HUMAN	TCR_STAAU	UHPC_ECOLI	Y098_MYCPN	ISP4_SCHPO	UHPC_SALTY	YUBA_BACSU	PAR2_MOUSE	NU5M_ASCSU	THIX_YEAST	ATR1_YEAST	YN86_YEAST	NU2M_ACACA	NU5M_RHISA	NUOH_RHOCA	NUSM_EQUAS	NU4M_BOVIN
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MVIN_BORBU	LACP_STAXY THT1_HUMAN C24B_BOVIN	ML1C_XENLA YWFA_BACSU	SGAT_ECOLI COX1_TRYBB	CYOB_BUCAI GUDP_ECOLI	YCD8_YEAST
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103 102.5	102 101.5 101.5	101 100.5	100.5	100.5	99.5
34 35	36 37 38	39 40	41	4 4	45

ALIGNMENTS

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-:- SUBCELLULAR LOCATION: Integral membrane protein:- STRUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, MAMMARY GLAND, -:- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, MAMMARY GLAND, -:- PTH: GLYCOSYLATED:- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS:- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license@isb-sib.ch). EMBL: UR1375; AAC51103.1; EMBL: AF079917; AAC62495.1; MIM; 602193;	بن	
-:-TISSUE SPECTICITY: EXPRESSED IN HEART, BRAIN, MAMMARY GLAND, ERYTHROCYTES AND PLACENTA, AND ALSO IN FETAL LIVER AND SPLEEN:-PTM: GLYCOSYLATED:-SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentiates requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL: U81375; AAC51103.1; EMBL: AF079117; AAC62495.1; MIM; 602193;	ري	SUBCELLULAR LOCATION: Integral membrane
LEXTHROCYTES AND PLACEBYTA, AND ALSO IN FETAL LIVER AND SPLEEN. -!- PTM: GLYCOSYLATED. -!- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS. -!- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatic the Buropean Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentiates requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license@isb-sib.ch). EMBL: ARC51103.1; EMBL: ARC51103.1; EMBL: ARC52495.1; MIM; 602193;	ပ္ (TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, MAMMARY
-!- FIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS!- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS. This SWISS-PROT entry is copyright. It is produced through a collaboral between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to licenseeisb-sib.ch). EMBL; U81375; AAC51103.1; EMBL; AR039117; AAC62495.1; MIM; 602193;	ب ر	ERYTHROCYTES AND PLACENTA, AND ALSO IN FETAL LIVER AND
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between the Sviss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/annout or send an email to license@isb-sib.ch). EMBL: 081375; AAC51103.1; EMBL: AF079117; AAC62495.1;	ب	This SWISS-PROT entry is copyright. It is produced through a collaborati
the European Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license@isb-sib.ch). EMBL; U81375; AAC51103.1; EMBL; AF079117; AAC62495.1;	ن	between the Swiss Institute of Bioinformatics and the EMBL outstation
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| GMFPAVTVEVKSSIAG----SSTWERYFIPVSCFLTFNIFDWLGRSLTAVFMWPGKDS
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9098E95E26515850 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 1.2e-16; 77; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 343.5;
Pred. No. 1.2
           Pfam; PF01733; Nucleoside_tran; 1.—
PRINTS; PR01130; DERENTRNSPRT.
ProDom; PD005103; DER_Nucleoside_tran; 1.
IPR002259; DER_Nucleoside_tran.
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                                                Transmembrane; Transport; Glycoprotein
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PRT;

STANDARD;

ENT2_HUMAN ID ENT2_HUMAN

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                                                                                                    nitrobenzylmercaptopurine riboside-insensitive nucleoside transporter) (Equilibrative NBMPR-insensitive nucleoside transporter) (Nucleoside transporter, ei-type) (36 Kba nucleolar protein HNP36) (Hydrophobic nucleolar protein, 36 kba) (Delayed-early response protein 12). SLC29A2 OR ENT2 OR HNP36 OR DER12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: BY PLATELET DERIVED GROWTH FACTOR (PDGF) AND FIBROBLAST GROWTH FACTOR (FGF).
SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved nucleolar protein.",
Biochem. Biophys. Res. Commun. 213:325-333(1995).
-!- FUNCTION: MEDIATES EQUILIBRATIVE TRANSPORT OF PURINE, PYRIMIDINE
NUCLEOSIDES AND THE PURINE BASE HYPOXANTHINE. LESS SENSITIVE THAN
SLC29A1 TO INHIBITION BY NITROBENZYLTHIOINOSINE (NBMPR),
DIPYRIDAMOLE, DILAZEP AND DRAFLAZINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. HNP36 ISOFORM IS
A NUCLEOLAR INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                       MEDITER 98148080; PubMed-9478986; Crawford C.R., Patel D.H., Naeve C., Belt J.A.; Crawford C.R., Patel D.H., Naeve C., Belt J.A.; "Cloning of the human equilibrative, nitrobenzylmercaptopurine riboside (NBMPR)-insensitive nucleoside transporter ei by functional expression in a transport-deficient cell line."; J. Blol. Chem. 273:5288-5293(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Placenta;
MEDLINE-98060726; PubMed-9396714;
Griffiths M., Yao S.Y., Abidi F., Phillips S.E., Cass C.E.,
Griffiths M., Daldwin S.A.,
Noung J.D., Baldwin S.A.,
"Molecular cloning and characterization of a nitrobenzylthioinosine-
insensitive (ei) equilibrative nucleoside transporter from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01/33; Nucreconstructions of PF01/33; Nucreconstructions of Probom; PD005103; DER_Nucleoside_tran; 1.
Nuclear protein; Transmembrane; Transport; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams J.B., Lanahan A.A.;
"A mammalian delayed-early response gene encodes HNP36, a novel,
               01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
Equilibrative nucleoside transporter 2 (Equilibrative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002259; DER_Nucleoside_tran.
Pfam; PF01733; Nucleoside_tran; 1.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Equilibrative nucleoside transporter 2 (Equilibrative
nitrobenzylmercaptopurine riboside-insensitive nucleoside transporter)
(Equilibrative NBMPR insensitive nucleoside transporter)
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                                                                                                                                                                                                                                                                           -----NFNNWVTLLSQLPLLLFTLLNSFLYQCVPETVRILG----SLLAILLLFALTAAL 116
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                            85; Gaps
                                                                                                                                                                                                                18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEXY-------VNYWFKPDGVE 62
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                                                                                        N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN ISOFORM HNP36).
                                                                                                                                                                        Length 456;
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AEF1B244397508E1 CRC64;
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                                                                                                                                                                       Score 326.5; DB 1;
Pred. No. 1.7e-15;
l; Mismatches 200;
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                                                                                                                                           50172 MW;
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22.98;
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SLC29A2 OR ENT2.
Rattus norvegicus (Rat).
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200
456 AA;
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SEQUENCE FROM N.A.
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CONFLICT
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Best Local
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STRAIN=SPRAGUE-DAWLEY; TISSUE=Jejunum;

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reen the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we
                                                                                                                                                                                        FUNCTION: MEDIATES BOTH INFLOX AND EFFLUX OF NUCLEOSIDES ACROSS THE MEMBRANE (EQUILIBRATIVE TRANSPORTER). IT IS INSENSITIVE (EI) TO LOW CONCENTRATIONS OF THE INHIBITOR NITROBENZYLMERCAPTOPURINE RIBOSIDE (NBMPR) AND IS SODIUM-INDEPENDENT. SPECIFIC FOR NUCLEOSIDES, BUT MAY ALSO TRANSPORT HYPOXANTHINE. MAY ALSO PLAY A ROLE IN THE EFFLUX OF INOSINE AND HYPOXANTHINE FROM MUSCLE CELLS DURING THE NET DEGRADATION OF PURINE NUCLEOTIDES THAT OCCURS DURING STRENHOUS EXERCISE AND/OR IN THE REUPTAKE OF THESE PURINES DURING THE RECOVERY PROCESS (BY SIMILARITY).
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                                                                                                                    (ei) equilibrative nucleoside transporter proteins (rENT1 and rENT2) from rat tissues.";
J. Biol. Chem. 272:28423-28430(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
MISCELLANEOUS: RESISTANT TO DIPYRIDAMOLE AND DILAZEP INHIBITION
(ANTICANCER CHEMOTHERAPEUTICS DRUGS).
                      Yao S.Y.M., Ng A.M.L., Muzyka W.R., Griffiths M., Cass C.E.,
Baldwin S.A., Young J.D.;
"Molecular cloning and functional characterization of
nitrobenzylthioinosine (NBMPR)-sensitive (es) and NBMPR-insensitive
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS
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CYTOPLASMIC (POTENTIAL).
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Pfam; PF01733; Nucleoside_tran; 1.
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MEDLINE=98019212; PubMed=9353301;
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297 VLVFTVTLSVFPALTAMVTTSSNS-----PGKWSQFFNPICCFLLFNVMDWLGRSLTSY 350
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                                                                                                 GLFFSITMASVWFINSFCAVLQGSLFGQLGTMPSTYSTLFLSGQGLAGIFAALAMLTSLA 182
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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nitrobenzylthioinosine (NBMPR)-sensitive (es) and NBMPR-insensitive
(ei) equilibrative nucleoside transporter proteins (rENT1 and rENT2)
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-!- FUNCTION: MEDIAFIES BOTH INFLOX AND EFFLUX OF NUCLEOSIDES ACROSS
THE MEMBRANE (EQUILIBRATIVE TRANSPORTER). IT IS SENSITIVE (ES) I LOW CONCENTRATIONS OF THE INHIBITOR NITROBENZYLMERCAPTOPURINE
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Equilibrative nucleoside transporter 1 (Equilibrative nitrobenzylmercaptopurine riboside-sensitive nucleoside transporter (Equilibrative NBMPR-sensitive nucleoside transporter)
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                                                            SWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGL ----LITVVK
                                                                                                                                            185 IGVTYFLNDEPKLVAIVYF---GISLVILLVCAIAL-----FFITKQ------
                                                                                                                                                                                                                             224 - DFYHYHHQKGMEIR------EK-----AETDRPSPSILWTTFTNCYGQLFNV
                                                                                                                                                                                                                                                               237 AELLGADEKNGIPVSPQQAGPTLDLDPEKELELGLEEPQKPGKPSVFVVFRKIWLTALCL
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SUBCELLULAR LOCATION: INTEGRAI MEMBRANE PIOTEIN.
TISSUE SPECIFICITY: EXPRESSED IN JEJENUM, LIVER AND LUNG.
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Yao S.Y.M., Ng A.M.L., Muzyka W.R., Griffiths M., Cass C.E.,
Baldwin S.A., Young J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AGFFTSVAMICAVASGSKLSESAFGYFIT----ACAVV-----ILAILCYLALPWM--- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            6 PQDRYKAVWLIFFVLGLGTLLPWNFFIT-ATQYFTSRLNTSQNISLVTNQSCESTEALAD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGV----ETWYSKEFMGS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 CGLLITVVKI-------GVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WITFINCYGQLFNVWFCFAVTLIIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV
                                                                                                                                                                                                                                                                                                              EXTRACELULAR (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                         Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                             84; Mismatches 191; Indels
                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 -LINKED (GLCNAC. . .) (P. A34CE92C20836D9B CRC64;
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                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                               CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 301; DB 1; 22.3%; Pred. No. 9.3e-14;
                                                                      BY SIMILARITY
       EMBL; AF015304; AAB88049.1; -.
InterPro; IPR002259; DER Nucleoside_tran.
Pfam; PF01733; Nucleoside_tran; 1.
PRIMYS; PR01130; DERENTRUSPET.
ProDom; PD005103; DER_Nucleoside_tran; 1.
                                                                                                                POTENTIAL.
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                                                             Transmembrane; Transport; Glycoprotein
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322
332
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                                                                                                                                                                                                                                                                                                                                               53
456 AA;
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29
82
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311
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GV-----DAQTSALGYFITPCVGILLSIVCYLSLPHLKFARYYLTEKLSQAPTQELETK 108
                      QDFYHYHHQKGMEIR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                             OR YAL022C
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                                                                                                                                                                                                                            FU26_YEAST
ID FU26_YEAST
AC P31381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                              01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Equilibrative nucleoside transporter 2 (Equilibrative
nitrobenzylmercaptopurine riboside-insensitive nucleoside transporter)
(Equilibrative NBMPR-insensitive nucleoside transporter)
transporter, ei-type) (36 KDa nucleolar protein HNP36) (Hydrophobic nucleolar protein, 38 KDa) (Delayed-early response protein 12).
SIC29A2 OR ENTZ OR HNP36 OR DER12.
                                                                                                                                                                                                                                                                                                                                                                             -! - INDUCTION: BY PLATELET DERIVED GROWTH FACTOR (PDGF) AND FIBROBLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 WFFWTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKI---- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TK 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM AND A SHORT FORM/HNP36 (SHOWN HERE); SEEMS TO BE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                          STRAIN-BAIB/C; TISSUB-Fibroblast;
MEDLINE-95367016; PubMed-7639753;
Williams J.B., Lanahan A.A.;
"A mammalian delayed-early response gene encodes HNP36, a novel,
                                                                                                                                                                                                                                                                       conserved nucleolar protein.;
Biochem. Biophys. Res. Commun. 213:325-333(1995).
-! FUNCTION: MEDIATES EQUILIBRATIVE TRANSPORT OF DURINE AND PYRIMIDIEN BUCLEOSIDES, AND THE PURINE BASE HYDOXANTHINE.
-! SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR. INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.1%; Score 209.5; DB 1; Length 327; 22.4%; Pred. No. 1.1e-07; Ive 49; Mismatches 134; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                              GROWTH FACTOR (FGF).
-!- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS.
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                                327 AA.
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                                PRT;
                                                       Created)
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                                STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         GROWTH FACTOR
                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   SPLICING
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Best Local Simi
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                             ENT2_MOUSE
Q61672;
                                                     01-NOV-1997
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TRANSMEM
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         RESULT 5
ENT2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 TSYFLWPDEDSQQLLPLLVCLRFLFVPLFMLCHVPQHAR-LPIIFRQDAYFITFMLLFAV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDIATE=9320532; PubMed=8458570;
Ouellette B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W.,
Cang B., Fortin N., Delaney S., Barton A.B., Raback D.B., Bussey H.;
"Sequencing of chromosome I from Saccharomyces cerevisiae: analysis of a 32 kb region between the LTE1 and SP07 genes:";
                                                           109 AELLQADEKNGVPISPQQASPTLDLDPEKEPEPEEPQKPGKPSVFVVFRKIWLTALCLVL
                                                                                                                                                                                      169 VFTVTLSVFPAITAMVTTSSNSPGKWGLFFNPI------CCFLLFNVMDWLGRSL
---EKAETDRPSPSILWTTFTNCYGQLFNVWF
                                                                                                                          CFAVILIIFPVM--MTVTTRGDSG----FLNKIMSENDEIYTLLTSFLVFNLFAAIGSIV
                                                                                                                                                                                                                                                        ASKIHWP---TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                        SHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 AA
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EMBL; L05027; AAA70393.1; -.
PIR; S36712; S36712.
SGD; S0000020; FUNG.
InterPro; IPR002259; DER_Nucleoside_tran.
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ProDom; PD005103; DER_Nucleoside_tran; 1.
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleoside transporter FUN26.
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLING-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                        128 SMSWFFWVTLGMATSI-NFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIG 186
                                                                                                                                                                                                                                                                                                                                                                                                                172 -PKWFNFMFIMMLVVISSMGTAMTQNGIMAIANVFGSEYSQGVWVGQAVAGVLPSLVLFA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 KYLVLSIFTTFVVTL-VFPVFASAT----YVTGLPLSNAQYIPLI--FTLWNLGDLYG 392
                                                                                                                                                                                                                                                                                   80 PNASINVFNLFL------IIAGPLIYR--VFAPVCFNIVNLTIILILVIVLEPTED 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 SLRSNEEEIRIVGRIDQMEDEDHRRTNGTRDDNDEGEELQLKVPFE------VLFAKL 341
                                                                                                                                                                                                                                    Gaps
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LAFIENSSVSTTGGILLYFFTTTLVVTIC-VVMFSVSKISRKVNENWNVEDGHITDVLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------QDFYHYH------QDFYHYH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 YGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIG
                                                                                                                                                                                                                                                                                                                                                         -----FHIYLAKRQYKYSRRVING-LVWEIIVFTVMCF----FTILHFLL-----
                                                                                                                                                                                                                                  Indels 117;
                                                                                                                                                                                                     Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                        POTENTIAL. 43C92A3E9A3D8D50 CRC64;
                                                                                                                                                                                                 Score 182.5; 'DB 1;
Pred. No. 1.2e-05;
9; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 VTYFLNDEPKLVA--IVYFGISLVILLVCAIALFFITK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIVASKIHWP-----TPRYLKFAIILRALFIPFF 346
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
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19.9%; Pre
tive 69;
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136
1171
1194
2334
263
364
431
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492
517 AA;
                                                                                                                                                                                                                    3est Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-2190;
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                                                                                                                                                                                                                                 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y672_METJA
Q58086;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 SKEFMG-----SLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILV 119
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              protein (Potential). FAMILY OF TRANSPORTERS.
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                                                                                                                                                                                                                                                       Hypothetical protein; Transmembrane; Transport; Complete proteome.
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80; Mismatches 1
              SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO THE NADC/P/PHO87
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19.1%; Pred. No. 0
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FE; PS01271; NA_SULFATE; 1
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Science 273:1058-1073(1996).
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TIGR; MJ0672; -.
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                                        NADC SUBFAMILY
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                                                                                                                                                                               STRAIN=RD / KW20 / ATCC 51907;

MEDLINE=9350630; PubMed=7542800;

Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

    -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING-
                                                                                                                                                                                                                                                                                                                                                                                                                        Sanders J.D., Cope L.D., Hansen E.J.; "Identification of a locus involved in the utilization of iron by Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 62:4515-4525(1994).
-!- FUNCTION: INVOLVED IN A PERIPLASMIC BINDING-PROTEIN-DEPENDENT
IRON(III) TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BII
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                               'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport; Iron transport; Transmembrane; Inner membrane;
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Pfam; PF00528; BPD_transp; 2.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
          HITB_HAEIN STANDARD; PRT; 506 AA. P71338; 053440; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) 1ron(III)-transport system permease protein hitB. HITB OR HIT0098.
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MEDLINE=95012644; PubMed=7927717;
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Science 269:496-512(1995)
                                                                                                     Haemophilus influenzae
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                                                                                                                                                                                              Gaps
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NIDJett D., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (OCT-1955) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HIGH-AFPINITY TRANSPORTER FOR EXTERNAL INORGANIC
PHOSPHATE (BY SIMILARITY):
-!- SUBCLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY: STRONG, TEAST PHO84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 LFFITKQDFYHYHQKGMEIREKAETDRPSPSILWTTFTNCYGQ-----LFNVWFCFAV
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                                                                                                                                                                                              167;
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                                                                                                                                                 Length 506;
                                                                                                                                                                                              Indels
G -> C (IN STRAIN TN106).
V -> G (IN STRAIN TN106).
S -> F (IN STRAIN TN106).
T -> M (IN STRAIN TN106).
ADA28861C1481A1D CRC64;
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Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                              69; Mismatches 144;
                                                                                                                                                 5.4%; Score 124.5; Di 21.6%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLI-----GNNICGLLITVVKIGVTYFLNDEP------KLVAI--VYFGISLVILL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LVLIPRLTMKESKSYEQSKALNKYTDNDTYIADDDEPKKDNQNVVEEKQINLTTSSDSHP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNKI--MSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWPT----PRYLKFAIILRALFI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKAIGFSSGKNEYHTLMRG-AIGNLIIAIAGYVPG--YWFTVFLVEKLGRKWIQLQGLFI 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 TSTEDFGDKRASTVPTSENTSGFIEYFSQWHHFKHLLATAVSWFLLDIAFYGVNLNOSVI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YMLVI-----LVGFG----VLLPWNMFI--TIAPEYYVNYWFKPDGVETWYSKEFMGSL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|| : | :|| :| | :| | HILGLTKREFKLMGFAGAGFFLDSYDLFIINLVSPIYEYLYWGGLEGKKPHYPSGIHG-- 91
                                                                                                                                                                               Phosphate transport; Transport; Transmembrane.
5 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCAI-----ALFFITKQDFY------HYHHQKGMEIREKAET--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 117.5; DB 1; Length 559; 20.1%; Pred. No. 0.35;
                                                                                                                                                                                                                                                                                      4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
9 (POTENTIAL).
5 (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
5 (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
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2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
EXTRACELLUIAN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
2E8958F86C2092E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                      InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PS0021E; PS0016; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62316 MW;
                                                                                                            EMBL; Z64354; CAA91247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                              Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                   Best Local Sim
Matches 101;
                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Weidman J.F., Sandek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
344 PFFFFCNYRVQTRAYPVFFESTDIFVIGG-----IAMSFSHGYLSALAMGYTPNVVPSH 397
                                F -> V (IN REF. 2).
DMQSLIMPNVI -> EYAKLNYAQCY (IN REF. 2).
3FCCDD95A2C35684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                   Y098_MYCGE STANDARD; PRT; 477 AA. P47344; Q49231; Q49509; 01-0cr-1996 (Rel. 34, created) 1-0cr-1996 (Rel. 34, Last sequence update) 16-0cr-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 46-155 AND 278-382 FROM N.A.
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STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; Pubmed=755993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR003837; Glu-tRNAGln.
Pfam; PF02686; Glu-tRNAGln; 1.
Hypothetical protein; Transmemhrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                luencing.";
Bacteriol. 175:7918-7930(1993)
                                                                                                                                                                469 VRGTAHGLSAALGKCGAILASL 490
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EMBL; U01701; AAB01013.1; -.
EMBL; U01782; AAD12771.1; -.
                                                                                                            398 YSRFAAQLSVCTLMVGLLTGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein MG098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma genitalium.
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108
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171
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477 AA;
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                                           20;
                                                                                                                                                         TTIAMIIAVAVSVVLVLMALAGGLTAALFRGYPGFRVTLELILVKISGL-----LF 109
                                                                                                                                                                                         134 WVTLGM--ATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLL------ 179
                                                                                                                                                                                                          -----ITVVKIG------PTYFL------NDE------PK 196
                                                                                                                                                                                                                                                                                                          197 LVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEIREKABTDRPSPSILWTTFTN 256
                                                                                                                               74 TIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILLILVIVLEPTEDSMSWFF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                371
                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 IPIFDTQ---TTGQTYDFWLLVRLLFAPLIFLLDIIV---IYPILLLTPIMLKGFKTVA 358
                                           Gaps
                                                                      22 YNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEF------MGSL 73
                                                                                                   ----YLFFKNILFLFFKRYPKNTPKIGVSNI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warner S.J., Lomax M.I.; "Evolution of the TM9 super family of membrane spanning proteins."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               YVQIIFYFAMVVIITMVVLYFVWIIKQKHFNYAYSKFFFRRYKHANHQFTLFVL--TKEN
                                                                                                                                                                                                                                                                           164 KTLSDFAYLVLSVGMVFASFLVTQFFVISVTQNLSAFQSNDQIVLRFNASPLNFSISLQR
                                                                                                                                                                                                                                                                                                                                                                    CYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAI
                                                                                                                                                                                                                                                                                                                                                                                        GSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE NONASPANIN (TM9SF) FAMILY.
                                            163;
               Length 477;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transmembrane 9 superfamily protein member 3 precursor.
               DB 1;
                                         70; Mismatches 130;
            Score 113.5; Di
Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 SETQTKGIKKSFSD--MOSLIM---PNVI-SH 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 -----GIAMSFSHGYLSALAMGYTPNVVPSH 397
                                                                                                                                                                                                                                                                                                                                                                                                282 WFYLILNV------ITLAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF269151; AAF98160.1; -. EMBL; BC004799; AAH04799.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last anno
            4.98;
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                                                                                          | | :|:|:|
20 YFAVVFLIIIV------
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                           Similarity
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                                         68;
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Q9ET30;
             Query Match
Best Local S
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                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 GVGGD---FPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKLVAIVY-----FGI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 SLVILLVCAIALFFITKQDFY-----HYHHQKGMEIREKAETDRPSPSILW---TTFTN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --TMVAVCCICFFVILPLNLVGTILGRNLSGQPNFPCRVNA-VPRPIPEKKWFMEPAVIV 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FNVWECFAVTLTIFPVMMTVTTRGDSGFLNKIMSEN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEIYTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --CVTIVCTYFLLN------AEDYRWQWTSFLSAA--STAIYVYMYSFYYYFFKTKM 541
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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EMBL/GenBank/DDBJ databases.
                                                                                                      POTENTIAL.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 ARQGGRRWIKQMFIGAFLIPAMVC-----GTAFFIN----FIAIYYHASRAIPFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gu J., Gu W., Jiang C., Yu Y., Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T953_HUMAN STANDARD; PRT; 589 AA.
T953_LUMAN STANDARD; O9P0G9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
binding protein) (EP70-P-iso).
TM9SE3 OR SMBP.
                                                                         PRANSMEMBRANE 9 SUPERFAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                         Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .) (P)
22FD4F8588FEC2AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                            49; Mismatches 127;
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                                                                                                                                                                                                                                                                                                                                                                     4.9%; Score 113.5; D. 18.2%; Pred. No. 0.69;
                                                                                            MEMBER 3.
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Gu Y., Peng Y., Li Y., Fu S.,
Wang Y., Chen Z., Fu G.;
                                                                                                                                                                                                                                                                                                                   67544 MW;
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"Evolution of the TM9 super
Submitted (MAY-2000) to the
IPR004240; EMP70.
                                                                                                                                                                                                                                                                                                                                                                                                          62; Conservative
                 Pfam; PF02990; EMP70; 1.
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312
312
3346
407
407
500
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1172
417
                                    Signal; Transmembrane.
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                                                                                                                                                                                                                                                         549
172
417
587 AA;
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Best Local Similarity
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us-08-816-011f-63.rsp

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Equus caballu
Mitochondrion
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P48656;
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                             298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                     Sugasawa T., Lenzen G., Simon S., Hidaka J., Cahen A., Guillaume J.L., Camoln L., Nahmias C., Strosberg A.D.; "The iodocyanopindolol and SM-11044 binding protein (SMBP) belongs to the emerging family of MP/D multispanning membrane proteins."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 PLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVY 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 ARQGGRRWIKQMFIGAFLIPAMVC-----GTAFFIN----FIAIYYHASRAIPFG- 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- TMVAVCCICFFVILPLNLVGTILGRNLSGQPNFPCRVNA-VPRPIPEKKWFMEPAVIV 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---FNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSEN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                         TRANSMEMBRANE 9 SUPERFAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
MISSING (IN REF. 2).
M -> I (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E673D547A35BC4A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9%; Score 113.5; Di
18.2%; Pred. No. 0.69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                              SEQUENCE OF 128-589 FROM N.A.
                  SEQUENCE OF 12-589 FROM N.A.
TISSUE-Skeletal muscle;
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502
539
571
174
419
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SIGNAL 1 28
CHAIN 29 589
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3294
3294
3360
3499
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TRANSMEM
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Matches
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                                                                                                                                            497 --CVTIVCTYFLLN-----AEDYRWQWTSFLSAA--STAIYVYMYSFYYYFFKTKM 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 TLKLSLSFKLD----YFSMIF-----VPVALFVTWSIMEFSLWYMHSDPYITRFFK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SMSWFFWVT------ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                   DEIYTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBL_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 IMLSIFNTY -- KNSTFPHHVKNTISYAFIT -- -- SLIPTMMFIHSGQETIISNWHWMTMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237;
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s; Mitochondrion.
5E794F1730235C10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                  572
                                                                                                                                                                                                         358 YPVFFESTDIFVIGGIAMSFSHGYLSAL------AMGY 389
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19.9%; Pred. No. 0.71;
ive 74; Mismatches 181;
                                                                                                                                                                                                                                                                     544 YGLF ------OTSFYFGYMAVFSTALGIMCGAIGY
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1_N.
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Pfam; PF00662; oxidored_q1_N; 1.
PRINTS; PR01434; NADHDHGNASE5.
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SECUENCE 604 AA; 68056 MW; SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
01-NOV-1997 (Rel. 35, Last ann
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Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caballus (Horse).
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332
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"Cloning and sequence analysis of the dnak gene region of Lactococcus
lactis subsp. lactis."; 2323-3263(1993).
J. Gen. Microbiol. 139:3253-3263(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASINVFNL-FLIIAGPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSWFFWVTLGMA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 KLSDYINIKKLLIIG-----ISLSCLGSLIAFI----GHNHFFILIFG-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.1 TSINFSNGLYENSVYGVG-GDFPHT--------YIGALL-----IGNNI 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 NVATIGNSVIFPGTMSVIVFGYFGGFLVDRKG-----SLFVFILGSLSIS----ISFL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 YSVLFWLCILSFFSVLN--EMVLNVSLPDIANHFNTTPGITNWVNTAYMLFSIGTAVYG 70
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P042377;
P01-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 70.0 kDa protein in dnam 3'region (ORF4).
Lactococcus lactis (subbsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaee;
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Transmembrane; Transport; Symport; Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FTTNYNWTFLILETI----
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 459;
                                                                                                                                                                                                                                                                                                                                    FE53C55535372B41 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 1;
Pred. No. 0.59;
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18.1%; Pred
7.9;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 FNIVNLTIILLIVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 QVIPQEDPNALSGEGXAW--NEFYG-----PLPTYFISVIK-FIVKSWSLSFSLFYSLC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .-----ICG-----ITMVKIGVT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AYPQGKWEPLYKIEFSYYKFPSLLFVFIVLFIFIFSLINFKKTNAKYSLIFS---CFSLV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 LIIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTS----FLVFNLFAAIG-----SIVAS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 KIHWPTPRYLKFALILRALFIPFFFCNYRVQTRAYPVF------FESTDIF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 ----WFKPDGVE----TWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIXRVFAPVC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 YFLNDEPKLVAIVYFGISLVILLVCAIALFF-------ITKQDFYH----- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 -NLKENIKIIGLGFLSVTSAİ----GLSAFFLFPLLENLKSGIYNVSNSDFSRSFGWNNI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 -YHHQKGMEIREKAETDRPSPSILWTTF------TNC-YGQLFNVWFCFAVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           16 KYNFEFYIIIL------FITILATFPFYRGNFHAGNDFAFNYARVMSTISALKDG 64
                                                                                                                                                                                                                                                                                     4.9%; Score 113; DB 1; Length 614;
19.3%; Pred. No. 0.78;
7ative 66; Mismatches 149; Indels 196;
                                                                                                                                                                               EMBL; X76642; CAA54090.1; -.
Hypothetical protein.
SEQUENCE 614 AA; 69869 MW; B1146136D09B89D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    21 KYNIVYWLVILVGFGVLLPWNMFITIA---PEYYVNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 AIG------EYLPQVIGSH 460
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Best Local Similarity 19.3#
Matches 98; Conservative
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Search completed: July 23, 2002, 16:43:23 Job time: 496 sec

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4.5 Compugen Ltd. version -GenCore Copyright (c) 1993

protein search, using sw model F protein ĕ

July 23, 2002, 15:41:32; Search time 44.23 Seconds (without alignments) 942.862 Million cell updates/sec Run on:

US-08-816-0116-2294 1 MVIINRSNTYAW

......LTGGLWPVVIEHFVDKPSIL 434 score: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000 Minimum Maximum

Post-processing: Minimum Match 0%

summaries Match 100% first 45 sun •• Database Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir4:*

	Description	hypothetical prote	hypothetical prote				Ψ		36k hydrophobic nu	hypothetical prote	ū	hypothetical prote	hypothetical prote		u	MDR-type permease			щ	hypothetical prote	sugar transport re	probable sugar ABC	Na+/H+-antiporter	iron (III) ABC tra	inorganic phosphat			conserved hypoteht	probable transport	DNA damage-inducib
SUMMARIES	ID	T16080	T28006	T23528	T23247	T01489	C86156	JC4196	JC4195	T21887	S36712	T22164	D85064	E85064	H64383	E97095	G96641	B90539	F83986	T21217	B90373	C95844	F89861	D64048	862503	F90285	H95041	A90013	B83601	C75053
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	Length	434	461	450	800	428	408	326	327	513	517	143	418	418	432	425	382	581	418	674	492	330	498	206	559	463	413	456	461	449
æ	Query Match	98.7		30.8	25.0		٠.	9.3		8.6	8.0	•			5.8	•	•	•	5.5	•	•	•	•	٠	•	•	5.0			5.0
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amino acid transpo eggshell protein p	NADH dehydrogenase tetracyclin resist	hypothetical prote hypothetical prote	Na+/H+-exchanging	Na+/H+-exchanging	proteinase-activat	regulatory protein	probable membrane	probable carbon st	probable integral	MG098 homolog G07_	isp4 protein - fis	hypothetical prote
H90507 H64210	T11867 S42238	S40085 E69143	A42111	B64459	S66518	RGECUC	S66834	A82294	A70814	873921	S45495	C85064
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446	604 459	614 694	383	388	397	440	497	464	419	479	176	394
5.0	4.4 0.0	4. 4. 9	4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8
114	$\frac{113.5}{113}$	$\frac{113}{112.5}$	112	111.5	111.5	111.5	111.5	111	110.5	110.5	110.5	110
30 31	33 33	34 35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

T16080

hypothetical protein F16H11.3 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000

Accession: T16080

submitted to the EMBL Data Library, April 1996
A Posserption: The sequence of C. elegans cosmid F16H11.
A; Reference number: Z18458
A; Accession: T16080

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA
A; Residues: 1-434 <MUX>
A; Residues: 1-434 <MUX>
A; Residues: 1-434 <MUX>
A; Cross-references: EMBL: 055376; NID: 91280130; PID: 91280131; PIDN: AAA98003.1; GSPDB: G
A; Experimental source: strain Bristol N2; clone F16H11
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Map position: X
A; Map position: X
A; Introns: 49/3; 94/2; 190/1; 256/3; 326/3; 392/2
C; Superfamily: Caenorhabditis elegans hypothetical protein ZK809.4

Gaps ö Length 434; Indels 4; ; 98.7%; Score 2265; DB 2; Llarity 99.1%; Pred. No. 2e-172; Conservative 0; Mismatches 4 Similarity 430; Query Match Best Local S. Matches 430

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099 qq

VETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVI 120 61 VETWYSKEFWGSLTIASQLPNASINVFNLFLLIAGPLIYRVFAPVCFNIVNLTILLLVI 120 61 Qγ ΩD

180 VLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLI 121 Qγ

180 Dp 240 240 TVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKODFYHYHQKGMEIREKA 181 181 qq Qγ

300 300 ETDRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEI 241 241 g ŏ

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301

361 FFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLW 420

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Query Match
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                                                                                                                                                                                                                                    Ribobson, R.
submitted to the EMBL Data Library, December 1995
A. Accession: T2806
A. Accession: T28006
A. Status: precliminary; translated from GB/EMBL/DDBJ
A. Status: precliminary; translated from GB/EMBL/DDBJ
A. Status: J461 <WIL>
A. Residues: 1461 <WIL>
A. Cross references: EMBL: Z68303; PIDN: CAA92642.1; GSPDB: GN00022; CESP: ZK809.4
A. Experimental source: clone ZK809
C. Genetics:
A. Genetics:
A. Genetics: A. Status: J10/2; 142/1; 357/3
C. Superfamily: Caenorhabditis elegans hypothetical protein ZK809.4
C. Superfamily: Caenorhabditis elegans
                                                                                                                                                                                    Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
Accession: T28006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein K09A9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-0ct-1999 #sequence_revision 15-oct-1999 #text_change 20-Jun-2000
C;Accession: T23528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TGVVTGYPTVYSSNFQSFQTIASQVPNLILINILINIFIUVVGGLASRI--TVGLSIVAVCV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 -----GVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 ILILVIVLEPPEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNN 174
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175 ICGLLITVVKI---GVTYFLNDEPKLVALVYFGISLVILLVCAIALFFITKQDFYHYHHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 KGMEIREK---AETDRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFP-VMMTVTTRGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 RAERQRNKNDEAVDSEGKVANYIATFKEAFPQLINVFLVFFVTLSIFPGVMMYVKDEKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-----FLNKIMSENDEI----YTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 FAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%; Score 716.5; DB 2; 35.8%; Pred. No. 2.2e-49; tive 86; Mismatches 167;
                                                                                                                                                                    hypothetical protein ZK809.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :: | :: |:::| | 425 VDPSKAQVAGMMAGFFLISGIVSGLIFTMVIKMVV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                   PVVIEHFVDKPSIL 434
                                                                     421 AVVIEHFVDKPSIL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim:
Matches 163;
                 361
                                                   421
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hypothetical protein KOZEII.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession. T23247
R; McMurray, A.
Submitted to the EMBL Data Library, July 1996
A; Reference number: 219715
A; Reference number: 219715
A; Reference number: 219715
A; Reference type: DNA
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-800 < WIL>
A; Residues: 1-800 < WIL>
A; Experimental source: clone K02EII
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 5
A; Il20/3; 137/1; 178/1; 280/3; 333/3; 418/3; 464/2; 496/1; 521/2;
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8
R; Swinburne, J.
submitted to the EMBL Data Library, August 1996
A; Reference number: 219753
A; Reference number: 219753
A; Accession: T2328
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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A; Residues: 1-450 WML>
A; Residues: 1-450 WML>
A; Residues: 1-450 WML>
A; Experimental source: clone K09A9
C; Genetics:
A; Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 IVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGDFPHTYIGALLIGNNICGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R---EKAETDRPSPSILWTFTNCYGQLFNVWFCFAVTLTIFP-VMMTVTTRGDSGFLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 IMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 VQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 ITVVKI---GVTYFLNDEPKLVALVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.8%; Score 706.5; DB 2; 36.0%; Pred. No. 1.3e-48; ive 88; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLLTGGLWPVVIEHFV 428
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GIVSGLIFTMVIKFVV 448
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Matches 157; Conserv
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242 260 302 355 360 415

303

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Chaccesion: C86156
RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chir, C.W.; Chug, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Schwiey, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-408 <STO>
A;Cross-references: GB:AE005172; NID:99972375; PIDN:AAG10625.1; GSPDB:GN00141
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                         SLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SCSVLVLVLWMTWNTRMSYRVRMNLGFS------MFIIAMMISPLID---W 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 VWKGEKGENVSYMLMVGSVVLCGLADGVVGGSLIGSAGKLPRQYMQAIFAGTASSGKPSF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ICGLLITVVKIGVTYFLNDEP---KLVAIVYFGISLVILLVCAIALFF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHKLPVMQQHLKFHQ------PLHSTLTIWMVGRKIKWPASGMLIIYSVTLSI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPVMMTVTTRGDSGFL-NKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VEQEAFPRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEFMG 71
DEP---KLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGME--IREKAE----T
                     243 DRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYT
                                                                                                                         ---EDVHS
                                                                                                                                                                   -LLTSF-----LVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQT
                                                                                                                                                                                           RAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.9%; Score 249.5; DB 2; Best Local Similarity 22.0%; Pred. No. 2.4e-12; Matches 99; Conservative 72; Mismatches 187;
                                                                                                    GLAWRTTLWDIVTKVKSHGFGIVLLYMVTLSIFPGYIT----
                                                                                                                                                                                                                                                                                                                                                            :| : | | | 418 SGSVIAWFWVI 428
                                                                                                                                                                                                                                                                                                                                    416 TGGL--WPVVI 424
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193
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A; Residues: 1-428 <VYS>
A; Residues: 1-428 <VYS>
A; Residues: 1-628 <VYS>
A; Residues: 1-628 <VYS>
A; Residues: 1-628 <VYS
Coss-references: EMBL: AC003671; NID: 92833627; PID: 93176684; GSPDB: GN00059; ATSP: F1707 C; Genetics: Cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F1707.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C:Accession: T01489
R:Vysotskala, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li tzt, D.; Ji, Y.; Palm, C.J.; Shina, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, Submitted to the EMBL Data Library, June 1998
A;Reference number: 214334
A;Reference number: 214334
A;Accession: T01489
A;Status: translated from GB/EMBL/DDBJ
A;Accession: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                     564
                                                                                                                                                                                                                                                                                                                                                                                                                                      254 FINCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLPNASINVFNLFLIIA-----GPLIYRVFAPVCFNIVNLTIILLLVIVLEPTEDSMSWF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILLILVIVLEPTEDSMSWFFWVTL 137
                                                                                                                                                                                                                                                                       GMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                            Gaps
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                                                                                               19 RDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFK-PDGVETWYSKEFMGSLTIGS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVETWYSKEFMGSLTIGS 77
                                                                                                                                                                                                                                                                                                          506 GTIVVLNAANGLEQNSMFGLASPFPFKYTNAVIIGQNFCGTAVTVLSM-LTKAASDDVQM
                                                                                                                                                                                                                                                                                                                                                                             198 VAIVYFGISLVILLVCAIALFFITKODFYHYHHOKGMEIREKAETDRPSPSILWTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQ--TRAYPVFFESTDIFVIG
                                                          23;
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                   Length 800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 GIAMSFSHGYLSALAMGYTPNVVPSH----YSRFAAQLSVCTLMVGLLTG 417
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                                                          Indels
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                 5;
                 Score 574.5; DB 2 Pred. No. 7.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 313.5; DB
Pred. No. 2.1e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Mismatches
                                                        88; Mismatches
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23.2%;
                 25.0%;
32.7%;
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                                                          Conservative
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                                    Similarity
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A;Map position: 1
A;Introns: 185/1
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Best Local Simi
Matches 100;
                                    Best Local Sim
Matches 134;
                                                                                                                                         388
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A Accession: JC4195
A; Molecule type: mRNA
A; Residues: 1-37 < WILL
A; Cross-references: EMBL: X86682; NID:9951302; PIDN:CAA60381.1; PID:9951303
C; Comment: This protein has a role in the growth response and participates in the pro
C; Genetics:
A; Genetics:
A; Start codon: AuG
C; Keywords: nucleoprotein; phosphoprotein
F; 82-159, Domain: hydrophilic: #status predicted < HYD>
F; 84,78 inding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F; 107/Msinding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
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Introns: 28/3; 56/1; 93/2; 163/3; 277/3; 314/1; 341/3; 384/2; 407/2; 458/2; 480/3
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Adte: 12.0ct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T21887
R;Steward, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: 219483
A;Accession: T21887
A;Accession: T21887
A;Accession: T21887
A;Accession: Pallminary; translated from GB/EMBL/DDBJ
A;Molecule Type: DNA
A;Residues: 1-513 < MLL>
A;Residues: EMBL:281078; PIDN:CAB03075.1; GSPDB:GN00019; CESP:F36H2.2
A;Experimental source: clone F36H2
C;Genetics: CESP:F36H2.2
A;Map Position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 WFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKI---- 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASKIHWP---TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSF 377
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:|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :|| 1 | :
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llarity 21.4%; Pred. No. 5e-08;
Conservative 77; Mismatches 159;
number: JC4195; MUID:95367016
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C;Species: Mus musculus (house mouse)
C;Date: 03-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 05-Nov-1999
C;Accession: JC4195
R;Williams, J.B.; Lanahan, A.A.
Biochem. Biophys. Res. Commun. 213, 325-333, 1995
A;Title: A mammalian delayed-early response gene encodes HNP36, a novel, conserved nucle
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-----GFIAENLKSQLLQSWYPILLITVYNISÔFVGKSLTALYLWQSIKSAT 321
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22.0%; Pred. No. 1.2e-09;
ilve 52; Mismatches 139;
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Db 172 -PKWFNFMFIAMLVVISSMGTAMTONGIMAIANVEGSEYSGGWWGGAVAGVLPSLVLFA 230 Oy 187 VTYELNDEPKLVAIVYEGISLVILLVCAIALFFITK	RESULT 11 722164 hypothetical protein F44D12.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T22164 R;Coles, L. submitted to the EMBL Data Library, December 1995	A; Reference number: 219525 A; Accession: T22164 A; Accession: T22164 A; Accession: T22164 A; Molecule type: DNA A; Residues: 1-143 <wil> A; Cross references: EMBL: 268298; PIDN: CAA92605.1; GSPDB: GN00022; CESP: F44D12.9 A; Experimental source: clone F44D12 C; Genetics: C; Genetics: A; Gene: CESP: F44D12.9 A; Map position: 4 A; Map position: 4 A; Introns: 19/1; 37/2</wil>	Query Match 7.8%; Score 180; DB 2; Length 143; Best Local Similarity 40.0%; Pred. No. 2.5e-07; Matches 32; Conservative 18; Mismatches 26; Indels 4; Gaps 1; Qy 14 QEAFPRDKYNIVYMLVILVGFGVLLPWNMFITIAPEXYVNWFKPDGVETWYSKEFMGSL 73 : : :: : :	Qy 74 TIGSQLPNASINVFNLFLII 93 1	C; Accession: D85064 R; Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Co Nature 402, 769-777, 1999 A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A; Reference number: A85001; MuID:20083488 A; Accession: D85064 A; Status: pre-liminary A; Molecule type: DNA A; Residues: 1-418 A; Residues: 1-418 A; Residues: 1-418 A; Cross-references: GB:NC_001268; NID:97267271; PIDN:CAB81054.1; GSPDB:GN00140 C; Genetics: A; Gene: AT4905120 A; Map position: 4
OY 81 NASINVENLELIIAGPLIYRVEAPVCENIVNLTIILILVIVULEPT 125 Db 62 TELQANPEAYLTVYGSIACVLGSILNVFATKSISNSTRMINGHILVVVVEIPTIALFF 119 OY 126EDSMSWFFWYLGMATSINF-SNGLYENSVYGVGGDFPHTYIGALLIGNNICGLIT 181 1 :	Qy 328 TPRYLKFAILLRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIG 371	RESULT 10 S36712 FUNZ6 protein - yeast (Saccharomyces cerevisiae) N:Alternate names: protein YAL022c C;Species: Saccharomyces cerevisiae C;Date: 31-Dec-1993 #sequence_revisiae C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Oct-1999 C;Accession: S36712 R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, submitted to the EMBL Data Library, January 1993 A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of A;Reference number: S36711	A;MCJECULE 1792. A;MCJECULE 1792. A;Residues: 1-517 <oue> A;Cross-references: EMBL:L05146; NID:g171851; PIDN:AAC04935.1; PID:g171853; MIP: C;Genetics: A;Gene: SGD:FUN26 A;Cross-references: SGD:S0000020; MIPS:YAL022c A;Map position: 1L C;Reywords: transmembrane protein</oue>	F;79-95/Domain: transmembrane #status predicted <tm1> F;155-171/Domain: transmembrane #status predicted <tm2> F;157-193/Domain: transmembrane #status predicted <tm3> F;218-234/Domain: transmembrane #status predicted <tm4> F;245-261/Domain: transmembrane #status predicted <tm4> F;344-360/Domain: transmembrane #status predicted <tm6> F;344-360/Domain: transmembrane #status predicted <tm6> F;412-428/Domain: transmembrane #status predicted <tm7> F;445-461/Domain: transmembrane #status predicted <tm7> F;500-516/Domain: transmembrane #status predicted <tm9></tm9></tm7></tm7></tm6></tm6></tm4></tm4></tm3></tm2></tm1>	Query Match 8.0%; Score 182.5; DB 2; Length 517; Best Local Similarity 19.3%; Pred. No. 6.5e-07; Matches 79; Conservative 69; Mismatches 131; Indels 117; Gaps 20; Qy 23 NIVYMLVILVGFGVLLPWNMFITIADEXYNVWFKPDGVETWSKBEFMGSLTIGSQL 79 1 1 1 1 1 1 1 1 1 1

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Chickestonia and so the second of the methanogenic archaeon, Methanoscould of the second of the methanogenic archaeon, M. C. J. White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak F. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Reference number: A64300; MUID:96337999
A; Accession: H64383
A; Accession: H64383
A; Accession: H64383
A; Accession: H64383
A; Cross-references: GB:U67514; GB:L77117; NID:92826304; PIDN:AAB98666.1; PID:91591386
C; Genetics: A; Apposition: REV598993-597695
C; Superfamily: probable transporter MJ0672
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C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 31-Dec-2000
                                                                                                                                                                                                              228 VADLAAAGIQNLSDLSDDDSKNQMLKKKELLLQN-----IDHAVNLFLIYVLTLSIFP-- 280
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                                                                                                                                                                  ------MEIREKAETD-----RPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFPVM
                                                                                                                                                                                                                                                                                                                                                       332 LKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTP
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                         VTYFL----NDEPKLVAIVYFGISLVILLVCAIALFFI-TKQDFYHYHHQKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 NVVPSHYSRFAAQLSVCTLM----VGLLTGGLW 420
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Special Protein Ar4905130 [imported] - Arabidopsis thaliana
C) Special Arabidopsis thaliana (mouse-ear cress)
C) Special Arabidopsis thaliana (mouse-ear cress)
C) Accession: E85064

R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Accession: E85064
A; Accession: E85064
A; Accession: E85064
A; Astatus: preliminary
A; Molecule type: DNA
A; Residues: 1-418 <ATO>
C; Genetics: 1-418 <ATO>
A; Cross-references: GB:NC_001268; NID:97267272; PIDN:CAB81055.1; GSPDB:GN00140
A; Map position: 4
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                                                                                            Gaps
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                                                                                                                                                              18 PRDKYNIVYWLVI----LVGFGVLLPWNMFITIAPEYY-VNYWFKPDGVETWYSKEF-MGS 72
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                         Length 418;
                                                                                        Indels
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69 ILILAYHESKINTRKRNLIGYIL-----
                                                                                        96; Conservative
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Matches 95; Conserv
                                                           Local Similarity
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RESULT 15
B97095
MDR-type permease [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97095
R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J; Barteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E97095
A;Cession: E97095
A;Residues: 1-425 ckUR>
A;Residues: 1-425 ckUR>
A;Coss-references: GB:AE001437; PIDN:AAK79552.1; PID:g15024539; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Genetics:
A;Genetics:
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331 YLKFAIILRALFIPFFFFCNYRVQTRAYPVFFEST----DIFVIGGIAMSFSHGYLSAL 385
                                155 YGVGGDFPHTYIGAL----LIGNNI----CGLLITVVKIGVTYFLNDEPKLVAIVYFGI 205
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5.7%; Score 130; DB 2; Length 425;
Best Local Similarity 22.7%; Pred. No. 0.0078;
Matches 94; Conservative 61; Mismatches 158; Indels 102;
                                                                                                                            390 PVGTPPNAI 398
                                                                                            386 AMGYTPNVV 394
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: amino acid
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                                                                                                                                                                                                                                                                July 23, 2002, 15:37:31; Search time 24.8 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-058-389A-2
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US-08-476-976-4
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APPLICANT: Crawford, Charles R.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A MITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
                                    13;
                                                                                                                                                                   272 LTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWP--TP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 IGSQLP--NASINVFNLFLIIAGPLIYRVFA------PVCFNIVN-----LTIILI 117
                                                                                                                                                                                                                 LVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICG 177
                                                                                                                                                                                                                                                                                                                                                          ---KGMEIREKAETDRPSPSILWTT-----FTNCYGQLFNVWFCFAVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYLKFAIILRALFIPFFFFCNYRVQTRAY-PVFFESTDIFVIGGIAMSFSHGYLSALAMG 388
                                      Gaps
                                                                                            |:|:| |: ::| |||||| |:| |:| |
7 PQDRYKAVWLIFFMLGIGTLLPWNFFMT-ATQYFTNRLDMSQNVSLVTAELSKDAQASAA 65
                                                                       18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEXYVNYWFKPDGVE---TWYSKEFMGSLT 74
                                                                                                                                                                                                                                                                                      178 LLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHQ-----
                                    59;
   Length 456;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | : | | : | 417 FGPKKVKPAEAETAGAIMAFFLCLGLALGAVFSFLFRAIV 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 YTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
15.0%; Score 343.5; DB 4; 24.3%; Pred. No. 3.6e-26; ive 77; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
RESISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/058,389A
FILING DATE: April 9, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09058389A Patent No. 6130065 GENERAL INFORMATION:
                                    Conservative
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COUNTRY: USA
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                Similarity
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                                    Matches 112;
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 Query Match
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APPLICANT: Belt, Judith A.
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NFNNWVTLLSQLPLLLFTLLNSFLYQCVPETVRILG----SLLAILLFALTAAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 EPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 QAQELETKAELLQSDENGIPSSPQKVALTLDLDLEKEPESEPDEPOKPGKPSVFTVFQKI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 YGQLENVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIVASKIHWP--TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAM 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 VKI-----GVTYFLNDEPKLVAIVYF---GISLVILLVCAIALFFITKQDFY---HYHHQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- ETDRPSPSILWTTFTNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 326.5; DB 4
22.9%; Pred. No. 1.8e-24;
Live 71; Mismatches 200
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TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                               LENGTH: 456 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 KGMEIREKA-----
                          TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 22.99
Matches 106; Conservative
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
DESCRIPTION: hENT2
HYPOTHETICAL: NO
                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
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PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ----NFNNWVILLSQLPLLLFTLLNSFLYQCVPETVRILG----SLLAILLEFALTAAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 EPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 VKI-----GVTYFLNDEPKLVAIVYF---GISLVILLVCAIALFFITKQDFY---HYHHQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 PRDSYHLVGISFFILGLGTLLPWNFFITAIPYFQARLAGAGNSTARILSTNHTGPEDAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 181; DB 4; Length 24; 23.6%; Pred. No. 2.7e-10; tive 42; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08097938
Patent No. 5629174
GENERAL INFORMATION:
APPLICANT: SUMDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
                                                                               ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,389A FILING DATE: APRIL 9, 1998 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYY------
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 134(FELECOMMINICATION IRPORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 247 amino acids TYPE: amino acid
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Best Local Similarity 23.69
Matches 59; Conservative
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TELEPHONE: 201-343-1684
                                        NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                          STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino a STRANDEDNESS:
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US-08-097-938-4
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APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 VAIVYF---GISLVILLVCAIALFFITKQDFY---HYHHQKGMEIREKA------ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: || : ::: :|| ::| ::| SALGYFITPPYVGILMSIVCYLSLPHEKRARYYLANKSSQAQAQELETKAELLQSDENGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 --------EIDRPSPSILWITFINCYGQLFNVWFCFAVILIIFPV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 MMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWP--TPRYLKFA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 IILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 INFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKI-----GVTYFLNDEPKL 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.3%; Score 214; DB 4; Length 326; 22.0%; Pred. No. 2e-13; Live 52; Mismatches 139; Indels
                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                           1340-1-013N
                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,389A
FILING DATE: APril 9, 1998
                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09058389A Patent No. 6130065
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                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 22.08
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
DESCRIPTION: hHNP36
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE
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AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR 63
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                                                                                              STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,000
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REGISTRATION NUMBER: 30,988
TITLE OF INVENTION: AND ANTAGONISTS, AND NUC. NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/TOCKET NUMBER: 2803-0006.20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 398 amino acids
amino acid
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Best Local S
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4.9%; Score 111.5; DB 1; Length 398;
Best Local Similarity 18.5%; Pred. No. 0.0045;
Matches 75; Conservative 54; Mismatches 131; Indels 145;
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APPLICANT: SCHNEDLIN, JOHAN
APPLICANT: SCANBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 ESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSV 407
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                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/097,938
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, D.C.
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ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGIETRATION UNDRER: 29,959
REFERENCE/DOCKET NUMBER: 22603
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 897-1500
TELEFAX: (202) 897-0763
TELEX: 90-4030
INFORMATION FOR SEO ID NO: 4:
SEGUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acids
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MOLECULE TYPE: protein

US-08-097-938-4
       CORRESPONDENCE ADDRESS:
                                                                                                   COUNTRY: USA
ZIP: 20006-1812
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APPLICANT: SCARBOROUGH, ROBERT M.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
ADDRESSEE: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
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                329 VALCLSTLNSCIDPFVYYFVSHDFRDHAKNALLCRSVRTVKQMQV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/476,976 FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2803-0006.20
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APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PR PROPER FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     Sequence 4, Application US/08476976 Patent No. 5874400
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity
Matches 75; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                     US-08-476-976-4
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STATE:
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                                                                                                                APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,840 FILING DATE:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 2803-0006...
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO: 4:
Sequence 4, Application US/08472840
Patent No. 5763575
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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                                                                            GENERAL INFORMATION:
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Sequence 4, Application US/08486673B Patent No. 6297026
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Best Local Similarity 18.5'
Matches 75; Conservative
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                                                                                                                                               293 VLAMYLI -- CF----
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CORGANISM: Homo sapiens
US-08-486-673B-4
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APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
APPLICANT: RARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
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                               303 LLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFF 362
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Pred. No. 0.0045;
!; Mismatches 131; Indels 145
                                                                                                 329 VALCLSTLNSCIDPFVYYFVSHDFRDHAKNALLCRSVRTVKQMQV 373
                                                                            363 ESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSV
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
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ER: 2803-0006.20
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APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 2803-0006.;
REGISTRATION NUMBER: 2803-0006.;
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURENT APPLICATION DATA::
APPLICATION NUMBER: US/408/414,410
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18.5%; Pred
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LENGTH: 398 amino acids
TYPE: amino acid
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Best Local Similarity 18.59
Matches 75; Conservative
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ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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CLASSIFICATION:
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COUNTRY:
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US-08-474-410-4
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|:: | |:
----IPAL---NITTCHDVLPEQLLV 237
                                                                                                                                                                                                       LLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFF 362
                                                                                                                                                                                                                                               61 VETWYS-KEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 WELILLVIIPLYVVKQTIF---------IPAL---NITICHDVLPEQLLV 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 VETVFSVDEFSASVLTGK-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 VYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEP-----KLVAIVYFGISLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GDMFNYFLSLAIGVFLFPAFLTA----SAYVLMIRMLRSSAMDENSEKKRKRAIKLIVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Mismatches 131; Indels 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sundellin, Johan
APPLICANT: Sundellin, Johan
APPLICANT: Scarborough, Robert M.
TITLE OF INVENTION: Nucleic Acids Encoding the C140 Receptor
FILE REFERENCE: 44481-5006-08-US
CURRENT APPLICATION NUMBER: US/08/486,673B
CURRENT FILING DATE: 1995-06-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US94/08536
PRIOR FILING DATE: 1994-07-26
NUMBER OF SEQ ID NOS: 63
                                                                                   GQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFL-----NKIMSENDE---
                                                                                                                                                                                                                                                                                                                             363 ESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSV 407
                                                                                                                                                                                                                                                                                                                                                                  329 VALCLSTLNSCIDPFVYYFVSHDFRDHAKNALLCRSVRTVKOMOV 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%; Score 111.5; DB .18.5%; Pred. No. 0.0045;
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GENERAL INFORMATION:

APPLICANT: SUNDELIN, JOHAN

APPLICANT: SCARBOROUGH, ROBERT M.

TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS

TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 115; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLIGNNICGLLITVVKIGVTYFLNDEP----KLVAIVYFGISLVI-LLVCAIAL-FFITK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 QDFYHYHHQKGMEIREKAETDRPSPSILWTTFTNCY------GQLFNVWFCFAVTLT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 IFPVMMTVTTRGDSGFL-----NKIMSENDE-----IYTLLTSFLVFNLFAAIG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| :| :| :| :| 253 LFPAFLTA----SAYVLMIRMLRSSAMDENSEKKRKRAIKLIVTVLAMYLI----- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 SIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 CFIPSNL-------LLVVHYFLIKSQGQSHVYALYIVALCLSTLNSCIDPF 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 FFYGNMYCSILFMTCLSVQRYWVIVNPMGHSRKKANIAIGISLAIWLLILLVTIPLYVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 QTIF-----IPAL---IPAL---NITTCHDVLPEQVLVGDMFNYFLSLAIGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.7%; Score 108.5; DB 1; Length 398;
19.2%; Pred. No. 0.009;
ive 59; Mismatches 141; Indels 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VETWYS-KEFMGSLTIGSQ----LPNASINVFNLFLIIAGPLIYRVFA---
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STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                               22803-20006.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 SHGYLSALAMGYTPNVVPSHYSRFAAQLSV 407
             COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOG/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,938
FILING DATE: 26-JUL-1993
CLASSIFFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08476000 Patent No. 5716789
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 -----LIG-FFYGNMYCSILFMTCLSVQRYWVIVNPMGHSRKKANIAIGISLAIWLLT 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 -----PVCFNIVNLTIILILVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 FLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVOTRAYPVFFESTD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.8%; Score 109.5; DB 4; Length 397;
Best Local Similarity 19.0%; Pred. No. 0.0071;
Matches 76; Conservative 57; Mismatches 131; Indels 137;
                                                                                                                APPLICANT: SCALBOLOGIA, Johan
APPLICANT: SCALBOLOGIA, Robert M.
TITLE OF INVENTION: NUCLEIC Acids Encoding the C140 Receptor
FILLE REFERENCE: 44481-5006-08-US
CURRENT APPLICATION NUMBER: US/08/486,673B
CURRENT APPLICATION NUMBER: US/08/097,938
PRIOR APPLICATION NUMBER: US 08/097,938
PRIOR PILING DATE: 1993-07-26
PRIOR FILING DATE: 1994-07-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VETWYS-KEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYR-VFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C140 RECEPTOR AND ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : | : : | : : | 332 LSTLNSCIDPFVYYFVSHDFRDHAKNALLCRSVRTVKQMQV 372
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
MORALSON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08097938
Patent No. 5629174
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOF
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
                : 08-486-673B-63
Sequence 63, Application US/08486673B
Patent No. 6297026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2000 Pennsylva CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20006-1812
                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-486-673B-63
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 63
LENGTH: 397
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AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 VEIVFSVDEFSASVLTGKLTTVFLPIVYIIVFVVGLPSNGMALW-VFLFRTKKKHPAVIY 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 SIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| :| :| :| :| :| :| :| 253 LFPAFLTA----SAYVLMIRMLRSSAMDENSEKRRRAIKLIVTVLAMYLI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.7%; Score 108.5; DB 1; Length 398; ilarity 19.2%; Pred. No. 0.009; Conservative 59; Mismatches 141; Indels 115;
                                                                                                                                                                                                                                                                                          SULTHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/472,840 FILING DATE:
                                 NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOREKIER
STREET: 2000 Pennsylvania Ave. N.W., Ste.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 VYYFVSHDFRDHAKNALLCRSVRTVKQMQV 373
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                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER: US/08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                           STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 75; Conserva
          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                 CITY: Was
STATE: D.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-476-976-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 IVNLTIILILVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 FFYGNMYCSILFMTCLSVQRYWVIVNPMGHSRKKANIAIGISLAIWLLILLVTIPLYVVK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 QDFYHYHQKGMEIREKAETDRPSPSILWTTFTNCY------GQLFNVWFCFAVTLT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 QTIF------IPAL---IPAL---NITICHDVLPEQVLVGDMFNYFLSLAIGVF 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 SIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAMSF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 108.5; DB 1; Length 398;
Pred. No. 0.009;
9; Mismatches 141; Indels 115;
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US-08-472-840-6
Sequence 6, Application US/08472840
Patent No. 5763575
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,000
FILING DATE: 07-JUN-1995
CLASSILEATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 35-JAN-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 2803-0006.20
FREISTRATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
FREISTRATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
FREINTH: 390 antho acids
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                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 19.2%;
Matches 75; Conservative 55
                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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     STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
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Sequence 6, Application US/08476976

Patent No. 5874400

GENERAL INFORMATION:

APPLICANT: SUNDELIN, JOHAN

APPLICANT: SCARBOROUGH, KOBERT M.

TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS

TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

CITY: Washington

STATE: D.C.
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4.7%; Score 108.5; DB 2; Length 398;
Best Local Similarity 19.2%; Pred. No. 0.009;
Matches 75; Conservative 59; Mismatches 141; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,976
FILING DATE: 07-010-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATORNEY/AGENT INFORMATION:
NAME: ADLER, REID G
REGISTRENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEFAX: (202) 887-0763
TELEFAX: 100-0430
TELEFAX: SEQUENCE CHARACTERISTICS:
LUNFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LUNFORMATION OCIDS
TELEGRAM: Aniho acids
TENENTH: 39 80 mniho acids
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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US-08-476-976-6
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Db 344 VYYFVSHDFRDHAKNALLCRSVRTVKQMQV 373
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Search completed: July 23, 2002, 16:35:03 Job time: 3452 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 23, 2002, 15:36:31; Search time 62.22 Seconds Run on:

(without alignments)
774.767 Million cell updates/sec

US-08-816-011F-63 2294 1 MVIINRSNTYAVEQEAFPRD......LTGGLMPVVIEHFVDKPSI¶ Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 Total number of hits satisfying chosen parameters: 747574 seqs, 111073796 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database :

| SIDSI/gcgdata/geneseqp_embl/AA1992_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1992_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1982_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1983_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1985_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1986_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1980_DAT:*
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| SIDSI/gcgdata/geneseqp_embl/AA1990_DAT:*
| SIDSI/gcgdata/geneseqqgeneseqp_embl/AA1990_DAT:*
| SIDSI/gcgdata/geneseqqgeneseqp_embl/AA1990_DAT:*
| SIDSI/gcgdata/geneseqqgeneseqp_embl/AA1990_DAT:*
| SIDSI/gcgdata/geneseqqgeneseqp_embl/AA1990_DAT:* ta/geneseq/geneseqp-embl/AA1980. ta/geneseq/geneseqp-embl/AA1981. A_Geneseq_032802:* .: /SIDS1/gcgdata

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		dР				
Result		Query				
NO.	Score	Match	Match Length DB	DB	ID	Description
1	2294	100.0	434	22	AAU07630	Caenorhabditis ele
7	2290	99.8	434	17	AAR92315	CORK potassium cha
m	645	28.1	458	22	ABB64784	Drosophila melanog
4	372.5	16.2	475	21	AAY82286	Rat ENT1 receptor
5	343.5	15.0	456	19	AAW69555	Human equilibrativ
9	343.5	15.0	456	21	AAB15520	Human ENT1 protein
7	327.5	14.3	475	21	AAY82285	Human ENT1 recepto
80	327.5	14.3	475	22	AAG67487	Amino acid sequenc
9	326.5	14.2	456	19	AAW83965	Equilibrative nucl
10	326.5	14.2	456	19	AAW69558	Human equilibrativ
11	326.5	14.2	456	21	AAB15517	Human NBMPR-1ENTP

Human PRO1380 (UNQ	Human PRO polypept	Protein of the inv	Rat equilibrative	Rat equilibrative	Human fibrosarcoma	Human protein sequ	Drosophila melanog	Drosophila melanog	Human HNP36 protei	Alternatively spli	Human NBMPR-IENTP	Polypeptide fragme	Human secreted pro	Human membrane or	Human immune/haema	Human immune/haema	Drosophila melanog	S. epidermidis ope	=	Putative P. abyssi	Human secreted pro	Human polypeptide,	Human protein sequ	Human secreted pro	Human secreted pro	ຜ	Human SM-11044-bin	Human SM-11044-bin	Human PAR-2 protei	Human C140 recepto	Human C140 recepto	Human secreted pro	Non-adrenergic SM
AAY99363	AAU29153	AAB66112	AAW69557	AAW69556	AAW64550	AAB93550	ABB65393	ABB68480	AAB15519	AAW83966	AAB15518	AAW89005	ABB51083	AAB88377	AAM85230	AAM90509	ABB62910	AAG82466	ABB64833	AAB96525	AAY76126	AAM93524	AAB92687	AAB75546	AAB75598	AAB94667	AAY82460	AAY82459	AAB35641	AAR66921	AAW01953	AAY94910	AAW61371
21	22	22	19	19	19	22	22	22	21	19	21	20	22	22	22	22	22	22	22	22	21	22	22	22	22	22	21	21	21	16	17	21	19
475	475	475	456	457	373	397	286	404	326	247	247	314	314	423	248	115	521	383	866	450	527	329	329	360	530	545	579	582	397	398	398	545	439
٠	14.2	4	4	ω.	11.9	1.	9.7			•	•		•		7.5							•	4.9				4.9				4.9	٠	4.8
326.5	326.5	326.5	320.5	301	272.5	261.5	221.5	217.5	214	181	181	180	180	179.5	172	125	124	119.5	117	114.5	114.5	113.5	113.5	113.5	113.5	113.5					111.5		111
12	13	14	15	16	17	18	19	20	21	22			25	56	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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61 VETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potassium channel genes from Drosophila melanogaster and Caenorhabditis elegans - useful in assaying substances to determine effects on cell growth, and in inhibiting nematode and insect pests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This potassium channel sequence is encoded by the CORK gene from Caenorhabditis elegans, and has 2 pore-forming domains situated between hydrophobic transmembrane helix domains. The CORK sequence contains structural features resembling pore-forming H5 domains contain the GY/Fe tripeptide motif required for potassium channels. 2 Putative pore-forming H5 domains selectivity. The protein contains 3 asparagine-linked glycosylation sites. The protein may be expressed in a heterologous host cell to assay substances to determine effects on cell growth. Potassium-agonists or potassium-antagonists identified by this method may be used as nematocides, anthelminthics or in therapy of cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVIINRSNTYAVEQEAFPRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORK; potassium channel; nematode; pore-forming domain;
transmembrane helix; N-glycosylation site; potassium-agonist;
potassium-antagonist; drug screening; nematocide; anthelminthic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2290; DB 17;
Pred. No. 2.2e-227;
                                                                                                                                                                                                                                                                                                                                                                                      domain"
                                                                                                                                                                                                                                                                                                                                                    note= "N-glycosylation site"
150..162
note= "Pore-forming H5 domair
                                                                                                                                                                                                                  'note= "N-glycosylation site"
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1; Mismatches
                                                                                                                                                                                                                                                                                                   81..83
/note= "N-glycosylation
                                                                                                                                                                                                                                            7note= "Pore-forming H5
                                                                                                                                                                                                                                                                                                                                                                                                                    "G-Y/F-G motif"
                                                                                                                                                                                                                                                                                    'note= "G-Y/F-G motif"
                                                                                                                                                                            Location/Qualifiers
5..7
                                    potassium channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                      /note= "P
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                                                                                                                                                      Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pausch MH, Price LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-239450/24.
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                                                                                                                       cardiac disorder.
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                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                     Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                    Modified-site
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   16-OCT-1996
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Matches 433;
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                                                                                                                                                                                                                             The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence
                                                                                                                                                    New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEIREKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETDRPSPSILMTTFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFESTDIFVIGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLW 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVIINRSNTYAVEQEAFPRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2294; DB 22; Length 434; Pred. No. 8.7e-228; Mismatches 0; Indels 0;
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                                                                                                                                                                                                   English.
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100.0%; Pre
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15-FEB-2000; 2000US-0503849
                                                                                                                                                                                                   Example 14; Fig 9; 131pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVVIEHFVDKPSIL 434
                                                                                                WPI; 2001-536570/59.
N-PSDB; AAS12162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 AA;
                                (BADI ) BASF CORP
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Matches 434;
                                                                 Pausch MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Rat; ENT1; ENTR1; immunosuppressant; vasotropic; thrombolytic; cytostatic; hypotensive; antiinflammatory; analgesic; anticoagulant; uncleoside transporter; ischaemia; cerebral embolism; malignant tumour; organ transplant rejection; renitis; pancreatitis; hypertension; analgesic; blood platelet coagulation inhibitor.
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                             IGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVLEPTEDSMSW--- 131
                                                                                                                                                                                                                                                            | | ||||: ||||:|| ||||284 qifkkaapqlfnifltffvtlsvfpaiqsnvhrsdpnfv----vgpdyftlvtcfatfn 338
                                                                                                                                                                                                                                                                                                                                                                                                   LFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNY--RVQTRAYPVFFESTDIFV 369
                                                                                                                                                                                                                                                                                                                                                                                                                            339 vfamlgslttswvqwpgprflwvpvvlrlafiplfvmcnyvppdsvrslavfiendwvyw 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 IGGIAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                          18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPD---GVETWYSKEFMGSLT
                                                                                                                                                         FFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFL
                                                                                                                                                                                                                                                                                                              NDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEIREKAETDRPSPSILW
                                                                                                                                                                                                                                                                                                                                                  252 TIFINCYGQLFNVWFCFAVILIIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                       Length 458;
                                                                                                                  Indels
                                                                                                                 178;
                                                                                      28.1%; Score 645; DB 22; 32.9%; Pred. No. 9.3e-58; ive 83; Mismatches 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82286 standard; Protein; 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kambe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENT1 receptor SEQ ID NO:5.
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                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-256588/22.
N-PSDB; AAA08030.
                                                                                                   Local Similarity
nes 138; Conserv
                                                  458 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp.
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                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                           TVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQKGMEIREKA 240
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                                                  YTLLTSFLVFNLFAAIGSIVASKIHWPTPRYLKFAIILRALFIPFFFFCNYRVQTRAYPV
                                                                                                                                                                                                      VLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLI
                                                                                                   ETDRPSPSILWTTFTNCYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEI
                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 21144; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 21144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EW.
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                                                                                                                                                                                                                                                                                                                                                                                    ABB64784 standard; Protein; 458 AA.
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11-JUL-2000; 2000US-0614150.
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from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                               PVVIEHFVDKPSIL 434
                                                                                                                                                                                                                                                                                                           New isolated nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                               ABB64784;
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                                                                                                The present invention describes human and rat ENTI receptors (ENTRI), with some amino-acids deleted, substituted or added, but which retain nucleoside transport activity, and can be used in drug development for agents in treating e.g. ischaemia, cerebral embolism, rejection in organ transport malignant tumours, renitis, pancreatitis and hypertension. The ENTRI proteins are nucleoside transporters which have vasotropic, immunosuppressant, thrombolytic, cytostatic, hypotensive, analgesic, antiliflammatory and anticoagulant activities. The transporter proteins, their DNA, oligonucleotides, transformants and antibodies can be used in drug development for agents in treating ischaemia, cerebral embolism, rejection in organ transplant, malignant tumours, renitis, pancreatitis, and hypertension, and as analgesics, or blood platelet coagulation inhibitors, as well as agents to reduce side-effects during chemotherapy. The present sequence represents the rat ENTRI protein.
                                                                                                                                                                                                                                                                                                                                                                                                     13;
Novel nucleoside transporter polypeptide, useful in drug development for agents in treating e.g. ischemia, cerebral embolism, rejection in organ transplant, malignant tumors, renitis, pancreatitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 NYWFK------PDGVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---fklrncsspasgkdpedadilnyfesylavastvpsllflvanfllvnrirvhvrvl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APVCFNIVNLTIILILVIVLEPTEDSMSW---FFWVTLGMATSINFSNGLYENSVYGVGG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 lpgleyaryymrpvvpihvfssedspprdapstssvapasravhtpplgpilkktaglgf 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 KIHWPTPR--YLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIF-VIGGIAMSFSH 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 wiqvpgprskllpilavsrvclvplfilcnyqprshltlvlfqs-diypilftcllglsn 426
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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21 snrheadgeallgkpldypapglgrpedrfngayiiffclgigggllpwnffvt-akeywa 79
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cavflyfitalifpaistnigpmhkgtgspwts---kfyvpltvfllfnfadlcgrqvta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; equilibrative nucleoside transporter; hENT1; hENT2; rENT1;
                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                      Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||| | : | | : : | : : : ||: |
gylstlvlmygpkivprelaeatsvvmlfymslglmlgsacaallehfi 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 GYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                                                                                                                                                                                                    209; Indels
                                                                                                                                                                                                                                                                                                                                                                     DB 21;
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                                                                                                                                                                                                                                                                                                                                                                   Score 372.5; DB 2
Pred. No. 1.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equilibrative nucleoside transporter 1.
                                                                                                                                                                                                                                                                                                                                                                                                  79; Mismatches
                                                                        Example 3; Page 81-83; 94pp; Japanese.
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25.6%;
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                                                                                                                                                                                                                                                                                                                             475 AA;
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The present sequence represents a substantially purified equilibrative nucleoside transporter (ENT), human ENT1 (hENT1). ENTS can transport a variety of purines and pyrimidines, including adenosine, uridine, guanosine, formycin B, tubercidin, and thymidine. ENTS are bidirectional, they transport a suitable permeant both into and out of cells. ENTS can be used as a tool for the development of new nucleoside drugs. Products from the present invention can be used for treating a subject having a disorder associated with an ENT. They can also be used with nucleoside drugs in the treatment of e.g. coronary or errebrowscular anoxia, viral infection or cancer. The products (e.g. antibodies and oligonucleotides hybridising to nucleic acid sequences encoding ENTS) can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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rENT2; coronary; cerebrovascular anoxia; viral infection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newly isolated equilibrative nucleoside transporter protein(s) gene(s) - used to develop products for treating disorder(s) associated with the transporter(s) and for use with nucleoside
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 IGSQLP--NASINVFNLFLIIAGPLIYRVFA---
                                                                                                                                                                                                                                                                                                                                                                                                                                              Young JD;
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96US-0034083
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nes 112; Conserv
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(UYLE-) UNIV
                                                      Homo sapiens
                                                                                                          W09829437-A2
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                                                                                                                                                                 09-JUL-1998
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13;

---PVCFNIVN----LTIILI 117

paaplpernslsaifnnvmtlcamlplllftylnsflhgripgsvrilgslvaillvfli 118 LVIVLEPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICG |::: |:: |:: | :: | :: | tailvkvqldalp-ffvitmikivlinsfgailggslfglagllpasytapimsgqglag

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IGSQLP -- NASINVFNLFLIIAGPLIYRVFA-----

184 231 271 303 329

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------KGMEIREKAETDRPSPSILWTT-----FTNCYGQLFNVWFCFAVT gegetkldliskgeepragkeesgysvsnsqptneshsikailknisvlafsvcfiftit

178 LLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAIALFFITKQDFYHYHHQ-----

388

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AAY82285 standard; Protein; 475

AAY82285

(first entry)

19-JUN-2000

AAY82285;

RYLKFAIILRALFIPFFFFCNYRVQTRAY-PVFFESTDIFVIGGIAMSFSHGYLSALAMG

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272 LTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIGSIVASKIHWP--TP 304 igmfpavtvevkssiag----sstweryfipvscfltfnifdwlgrsltavfmwpgkds

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The invention relates to the isolation of a gene encoding a NBMPR-IENTP (nitrobenzylmercaptopurineriboside-insensitive, equilibrative nucleoside transporter protein) from Hela cells. The protein transports nucleosides across the plasma membrane by a facilitated diffusion process and is arross the plasma membrane by a facilitated diffusion process and is involved in the proliferative response. The transporter is useful in screening to identify natural nucleoside permeants and/or their in thibitors or analogues, potential therapeutic agents, also for studies on protein structure and mechanian. Cells that express the iENTP as the only transporter protein are used for drug screening (especially to identify antitumour and antiviral nucleoside analogues), in chemotherapy of cancer and for selective expression of heterologous genes for gene therapy. The cDNA is used for recombinant expression of iENTP and as a source of oligonucleotides (diagnostic primers and probes, ribozymes and antisense sequences). Antibodies raised against iENTP are used for detection of the protein by usual immunoassays and as (ant)agonists of iENTP activity. This sequence represents the human ENTI protein and comparison with the human NBMPR-iENTP protein (AABISSI7).
                                                                                                                                                                                                                                                                                                                                                   Antiviral; antitumour; NBMPR-iENTP; nitrobenzylmercaptopurineriboside; insensitive, equilibrative nucleoside transporter protein; cancer; plasma membrane; facilitated diffusion; gene therapy; primer; probe.
New nucleic acid encoding nucleoside transporter, useful for drug screening to identify antitumour and antiviral agents and for gene
                                                          389 YTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                              417 fgpkkvkpaeaetagaimafflclglalgavfsflfraiv 456
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Pred. No. 1.1e-26;
7; Mismatches 212
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24.3%; Pred
a+ive 77;
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AAB15520
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Human; ENT1; ENTR1; immunosuppressant; vasotropic; thrombolytic; cytostatic; hypotensive; antiinflammatory; analgesic; anticoagulant; nucleoside transporter; ischaemia; cerebral embolism; malignant tumour; organ transplant rejection; rentiis; pancreatitis; hypertension; analgesic; blood platelet coagulation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes human and rat ENT1 receptors (ENTR1), with some amino-acids deleted, substituted or added, but which retain nucleoside transport activity, and can be used in drug development for agents in treating e.g. ischaemia, cerebral embolism, rejection in organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleoside transporter polypeptide, useful in drug development for agents in treating e.g. ischemia, cerebral embolism, rejection in organ transplant, malignant tumors, renitis, pancreatitis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakagawa
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Human ENT1 receptor SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kambe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK.
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                                                                                                                                                                                                                                                                                      Homo sapiens
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59;

212;

Conservative

112;

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Similarity

Local Best Loca Matches 18

DB 21; Length 456; Indels PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYVNYWFKPDGVE---TWYSKEFMGSLT 74 |:|:| |: :::| | |||||| |:| | :|: | pqdrykavwliffmlglgtllpwnffmt-atgyftnrldmsqnvslvtaelskdagasaa 65 16-MAY-2000; 2000US-0204725

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15;
transplant, malignant tumours, renitis, pancreatitis and hypertension. The ENTR1 proteins are nucleoside transporters which have vasotropic, immunosuppressant, thrombolytic, cytostatic, hypotensive, analgesic, antiinflammatory and anticoagulant activities. The transporter proteins, their DNA, oligonucleotides, transformants and antibodies can be used in drug development for agents in treating ischaemia, cerebral embolism, rejection in organ transplant, malignant tumours, renitis, pancreatitis and hypertension, and as analgesics, or blood platelet coagulation inhibitors, as well as agents to reduce side-effects during chemotherapy. The present sequence represents the human ENTR1 protein.
                                                                                                                                                                                                                                                                                                                                                                                         53 NYWFK-------PDGVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYR 100
                                                                                                                                                                                                                                                                                                                                                                                                                          80 ---fklrnssspatgedpegsd--ilnyfesylavastvpsmlclvanfllvnrvavhir 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 VFAPVCFNIVNLTIIILILVIVLEP--TEDSMSW---FFWVTLGMATSINFSNGLYENSVY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 GVGGDFPHTYIGALLIGNNICGLLITVVKIGVTYFLNDEPKLVAIVYFGISLVILLVCAI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 ALFFITKQDFYHY-----LWTTFTN 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 lcgrqltawiqvpgpnskalpgfvllrtcliplfvlcnyqprvhlktvvfqsdvypalls 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 lylllsrleyaryymrpvlaahvfsgee--elpqdslsapsvasrfidshtpplrpilkk 304
                                                                                                                                                                                                                                                                                                                    ---PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                                                                                                                                                                                                                                                                        CYGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSE--NDEIYTLLTSFLVFNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transporter protein; nucleoside transporter; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 IAMSFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTGGLWPVVIEHFV 428
                                                                                                                                                                                                                                                                                 75;
                                                                                                                                                                                                                                               Length 475;
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                                                                                                                                                                                                                                               DB 21;
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                                                                                                                                                                                                                                             Score 327.5; DB 21;
Pred. No. 5.3e-25;
3; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG67487 standard; Protein; 475
                                                                                                                                                                                                                                                                                 83;
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                                                                                                                                                                                                                                             14.3%;
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                                                                                                                                                                                                                                                                                                                    7 SNTYAVEQEAF-----
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                              475 AA;
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                                                                                                                                                                                                                                                                                 Matches 116;
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15;
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                                                                       Hu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 NYWFK------PDGVETWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALFFITKQDFYHY------HHQKGMEIREKAETDRPSPSI------LWTTFTN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 lylllsrleyaryymrpvlaahvfsgee--elpgdslsapsvasrfidshtpplrpilkk 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SNTYAVEQEAF------PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ssslradgealleklldrpppglqrpedrfcgtyiiffslgigsllpwnffit-akeywm
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                                                                                                                                                                                   Novel nucleic acid sequences encoding the novel human transporter proteins useful for diagnosis, drug screening, clinical trial monitoring, and treatment of diseases and disorders .
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                                                                       Kieke JA,
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                                                                       Cullinan EB,
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                                                                       Zambrowicz B,
                                                                                                                                                                                                                                                            English
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                                                                                                                                                                                                                                                        Disclosure; Page 58-59; 61pp;
                                    (LEXI-) LEXICON GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               useful in gene therapy.
                                                                         Scoville J,
                                                                                        Walke DW;
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Best Local Similarity
Matches 116; Conserv
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                                                                       Donoho G,
Turner CA,
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AAW83965
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                                                                                                            WPI; 1998-594576/50.
N-PSDB; AAV69698.
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11-APR-1997;
                  Homo sapiens
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which is insensitive to nitrobenzylmercaptopurine riboside (NBMPR). Cells
transformed with a construct containing the iBNYP nucleic acid can be
used to produce the protein recombinantly. iENTP is used to identify
specific ligands (particularly antiviral and antitumour nucleoside
analogues that are preferentially transported into cells) and to raise
antibodies. Cells in which iENTP provides all available transport
antibodies. Cells in which iENTP permeants of iENTP and (b) to screen
specific inhibitors of iENTP (potential drugs). Fragments of the iENTP
cucleic acid are used, as probes, primers, antisense molecules, and
cribozymes for therapy or diagnosis, and knockout mice in which both
alleles encoding iENTP contain an inactivating defect are also useful for
drug screening. Cells that have been transduced with iENTP nucleic acid
ex vivo are used particularly, for cancer chemotherapy. Vectors in which
the iENTP gene is linked to a heterologous gene (e.g. encoding adenosine
che iENTP gene is linked to a heterologous gene (e.g. encoding adenosine
                                                                      Equilibrative nucleoside transport protein; iENTP; NBMPR; transport; nitrobenzylmercaptopurine riboside; antiviral; antitumour; screening; inhibitor; drug; knockout mice; cancer; chemotherapy; gene therapy; adenosine deaminase; factor VIII.
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                    Equilibrative nucleoside transport protein (iENTP).
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7note= "transmembrane domain TM10"
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te= "transmembrane domain TM8"
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                                                                                                                                                                                                                                                                       .ocation/Qualifiers
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97US-0838845
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                                                                                                      63 TWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVL 122
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                                                                                                                                                                                                                                                                                           231 qaqeletkaellqsdengipsspqkvaltldldlekepesepdepqkpgkpsvftvfqki 290
                                                                                                                                                                                                                                                                                                                    258 YGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIG 317
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                                                                                                                                                                                                                                                                                                                                                                         318 SIVASKIHWP--TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAM 375
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                                                    --- VNYWFKPDGVE 62
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                                                                                                                                                                                                              183 VKI----GVTYFLNDEPKLVAIVYF---GISLVILLVCAIALFFITKQDFY---HYHHQ
                                                                                                                                                                                                                                                                 -----ETDRPSPSILWTFTNC
                                                                                                                                                                                                                                                                                                                                     equilibrative nucleoside transporter; hENT1; hENT2; rENT1; coronary; cerebrovascular anoxia; viral infection; cancer.
                          85;
 Length 456;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             376 SFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG 417
DB 19;
14.2%; Score 326.5; DB 19; 22.9%; Pred. No. 6.3e-25; ive 71; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human equilibrative nucleoside transporter 2.
                                                    18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYY--
                                                                                                                                                                                                                                                                 232 KGMEIREKA------
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96US-0034083
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                          Matches 106; Conservative
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             Best Local Similarity
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30-DEC-1996;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                    nucleoside transporter (ENT), human ENT2 (hENT2). ENTS can transport a variety of purines and pyrimidines, including adenosine, uridine, guanosine, inosine, formycin B, tubericidin, and thymidine. ENTS are bidirectional, they transport a suitable permeant both into and out of cells. ENTS can be used as a tool for the development of new nucleoside drugs. Products from the present invention can be used for treating a subject having a disorder associated with an ENT. They can also be used with nucleoside drugs in the treatment of e.g. coronary or escentoroxicular anoxia, viral infection or cancer. The products (e.g. antibodies and oligonucleotides hybridising to nucleic acid sequences encoding ENTS) can also be used for detection and drug screening.
                                                                                                         present sequence represents a substantially purified equilibrative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiviral; antitumour; NBMDR-iENTP; nitrobenzylmercaptopurineriboside; insensitive, equilibrative nucleoside transporter protein; cancer; plasma membrane; facilitated diffusion; gene therapy; primer; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 EPTEDSMSWFFWVTLGMATSINFSNGLYENSVYGVGGDFPHTYIGALLIGNNICGLLITV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 TWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----nfnnwvtllsqlplllftllnsflygcvpetvrilg----sllailllfaltaal 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qaqeletkaellqsdengipsspqkvaltldldlekepesepdepqkpgkpsvftvfqki 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGQLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSENDEIYTLLTSFLVFNLFAAIG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 wltalclvlvftvtlsvfpaitamvtssts-----pgkwsqffnpiccfllfnimdwlg 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIVASKIHWP--TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 rsltsyflwpdedsrllpllvclrflfvplfmlchvpqrsr-lpilfpgdayfitfmllf 403
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              ----VNYWFKPDGVE 62
Newly isolated equilibrative nucleoside transporter protein(s) and gene(s) - used to develop products for treating disorder(s) associated with the transporter(s) and for use with nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || : || : :|| aml1smasgv-----daetsalgyfitpyvgilmsivcyls1ph1kfaryylankssga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 VKI-----GVTYFLNDEPKLVAIVYF---GISLVILLVCAIALFFITKQDFY---HYHHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ETDRPSPSILWTTFTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 vkvdmspgpffsitmasvcfinsfsavlqgslfgqlgtmpstystlflsgqglagifaal
                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                   Length 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 avsngylvsltmclaprqvlpherevagalmtfflalglscg 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG 417
                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                Score 326.5; DB 19;
Pred. No. 6.3e-25;
1; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                           18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYY---
                                                                                                                                                                                                                                                                                                                                                                             71;
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                                                                          Claim 5; Fig 20; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                14.28;
22.98;
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                       456 AA;
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Matches 106;
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                                              drug(s)
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This sequence represents nitrobenzylmercaptopurineriboside-insensitive, equilibrative nucleoside transporter protein (NBMPR-iENTP) isolated from HeLa cells. The protein transporter nucleosides across the plasma membrane by a facilitated diffusion process and is involved in the proliferative response. The transporter is useful in screening to identify natural thrapeutic agents also for studies on protein structure and mechanism. The appeutic agents, also for studies on protein structure and mechanism. Cells that express the IBNTP as the only transporter protein are used for drug screening (especially to identify antitumour and antiviral nucleoside analogues), in chemotherapy of cancer and for selective expression of heterologous genes for gene therapy. The cDNA is used for recombinant expression of iBNTP and as a source of oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (diagnostic primers and probes, ribozymes and antisense sequences). Antibodies raised against iENTP are used for detection of the protein by usual immunoassays and as (ant)agonists of iENTP activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIVASKIHWP--TPRYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGGIAM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYY-------VNYWFKPDGVE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding nucleoside transporter, useful for drug screening to identify antitumour and antiviral agents and for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TWYSKEFMGSLTIGSQLPNASINVFNLFLIIAGPLIYRVFAPVCFNIVNLTIILILVIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----nfnnwvtllsqlplllftllnsflyqcvpetvrilg----sllailllfaltaal
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                                                                                                                                                                                                                                                                                                                                                (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
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                                                                                                                                                                                                      98US-0058389
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nes 106; Conserv
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Homo sapiens.
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20-OCT-19
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 345 rsltsyflwpdedsrllpllvclrflfvplfmlchvpqrsr-lpilfpqdayfitfmllf 403
                                                                                                                                    Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
                                                                                                                      Human PRO1380 (UNQ717) amino acid sequence SEQ ID NO:79.
              376 SFSHGYLSALAMGYTPNVVPSHYSRFAAQLSVCTLMVGLLTG 417
                         AAY99363 standard; Protein; 475 AA
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98US-0100848.
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                                                                                                     08-AUG-2000 (first entry)
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02-SEP-1998

09-SEP-1998

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110-SEP-1998
                                                                                                                                                              Homo sapiens.
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15-SEP-1998;
15-SEP-1998;
16-SEP-1998;
16-SEP-1998;
16-SEP-1998;
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18-SEP-1998;
22-SEP-1998;
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23-SEP-1998;
23-SEP-1998;
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16-SEP-1998;
17-SEP-1998;
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18-SEP-1998;
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                                                                                                                                                                                             09-MAR-2000
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23-SEP-1998
                                                                                       AAY99363;
                                                       RESULT 12
                                                               AAY99363
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tumour; cancer; human; cattle; horse;

(first entry)

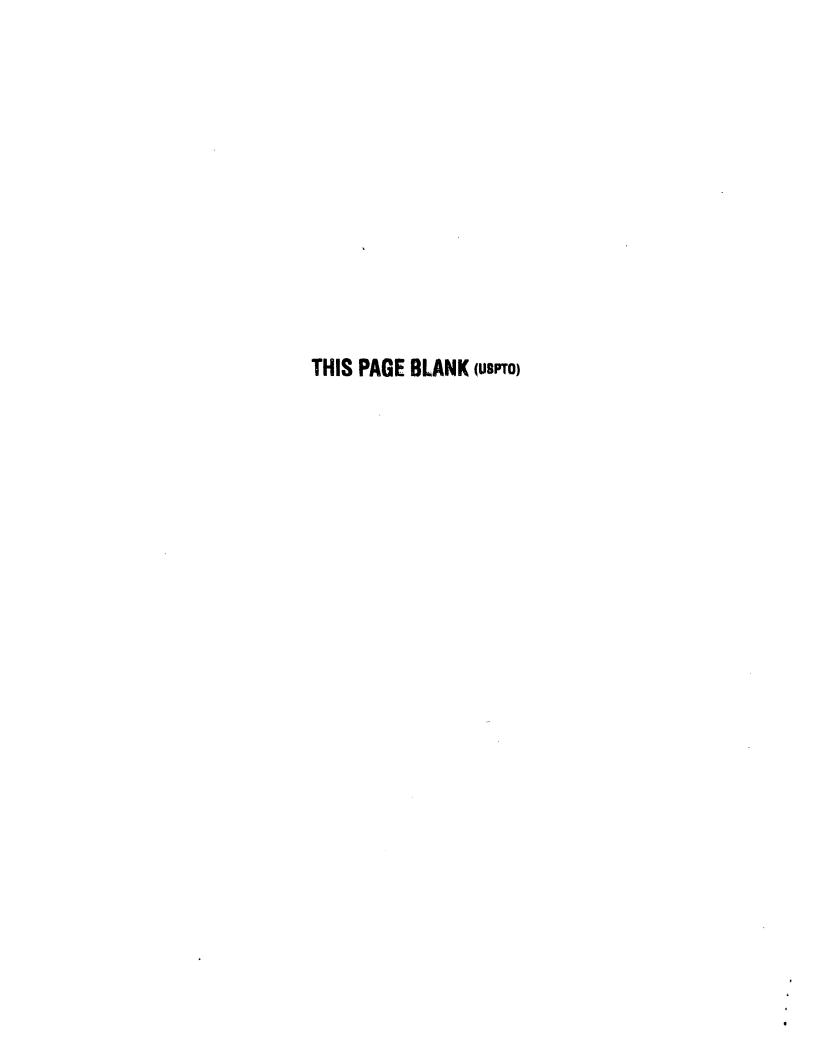
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dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                      Human PRO polypeptide sequence #130.
                                                                polypeptide; mammal;
                                                                                                                                               WO200168848-A2
                                                                                                                        Homo sapiens
                                                                                                                                                                                             28-FEB-2001;
                                                                                                                                                                                                                                            03-MAR-2000;
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               18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan J,
                                                              PRO
     15;
                                                                                                                                                                                                                                 The
                                                                                                                                                                                                                  AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO
                                                                                                                                                             ö
                                                                                                                                              New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gmtgsfpmrnsgalisggamggtvsavasl-vdlaassdvrnsalaffltatiflvlcmg 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 ALFFITKQDFYHY------HHQKGMEIREKAETDRPSPSI------LWTTFTN 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---fklrnssspatgedpegsd--ilnyfesylavastvpsmlclvanfllvnrvavhir 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 VFAPVCFNIVNLTIILLILVIVLEP--TEDSMSW---FFWVTLGMATSINFSNGLYENSVY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYGOLFNVWFCFAVTLTIFPVMMTVTTRGDSGFLNKIMSE--NDEIYTLLTSFLVFNLFA 314
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            SNTYAVEQEAF-------PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                           WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 AIGSIVASKIHWPTP---RYLKFAIILRALFIPFFFFCNYRVQTRAYPVFFESTDIFVIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 lcgrqltawiqvpgpnskalpgfvllrtcliplfvlcnyqprvhlktvvfqsdvypalls
                                                                                                                                                                                                                                                                                                                                                                                                   75;
                                                                                     Wood
                                                                                                                                                                                                                                                                                                                                                                             Length 475;
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                                                                                    Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                           Score 326.5; DB 21;
Pred. No. 6.7e-25;
; Mismatches 202;
                                                                                  Smith V,
                                                                                                                                                                                                                                                                                                                  polypeptides from the present invention
                                                                                     Gurney AL,
                                                                                                                                                                                            Claim 12; Fig 48; 773pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   83;
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                                                                                                                                                                                                                                                                                                                                                                           14.28;
24.48;
            98US-0108852.
98US-0108858.
 98US-0108851
                                    98US-0108904
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                                                            (GETH ) GENENTECH INC
                                                                                  Goddard A,
                                                                                                          2000-237871/20.
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                                                                                                                       N-PSDB; AAA37045
18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
                                    18-NOV-1998;
                                                                                    Baker K,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard A, Gor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Fig 260; 774pp; English.
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Watanabe CK, W
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2000W0-US08439.
2000US-194449P.
2000US-194647P.
2000US-195975P.
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2000US-199397P.
2000US-199550P.
2000US-199654P.
2000US-189320P.
2000US-189328P.
                                2000WO-US06884.
2000US-190828P.
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2000US-196187P.
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2000US-196820P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS46054
               14-MAR-2000;
15-MAR-2000;
21-MAR-2000;
                                                               21-MAR-2000;
21-MAR-2000;
21-MAR-2000;
                                                                                                                               29-MAR-2000;
29-MAR-2000;
30-MAR-2000;
                                                                                                                                                                               04-APR-2000;
04-APR-2000;
11-APR-2000;
11-APR-2000;
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11-APR-2000;
11-APR-2000;
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25-APR-2000;
03-MAY-2000;
17-MAY-2000;
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18-APR-2000;
                                                                                                                 28-MAR-2000;
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                detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation of tifferentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
    polypeptides and their associated nucleic acids can be used to
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                                                                                                                                                                                                                                                                                                                                                                      ; Score 326.5; DB 22; Length 475;
; Pred. No. 6.7e-25;
83; Mismatches 202; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:: :||| ||| ||| ||: | ssslradqealleklldrpppg|qrpedrfcgtyiiffslgigsllpwnffit-akeywm 79
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                                                                                                                                                                                                                                                                                                                                                                        14.2%;
24.4%;
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.4:
Matches 116; Conservative
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Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to secreted and transmembrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 SNTYAVEQEAF-------PRDKYNIVYWLVILVGFGVLLPWNMFITIAPEYYV 52
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21 ssslradqealleklldrpppglqrpedrfcgtyiiffslgigsllpwnfflt-akeywm
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Gurney AL, F
A, Tumas D;
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                                                                                                                                  99WO-US28313.
99WO-US28551.
99WO-US30095.
2000WO-US00219.
2000WO-US00376.
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                2000WO-US04342
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Gao W, Goddard A, Godowsk:
Pan J, Paoni NF, Roy MA,
Watanabe CK, Williams PM,
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Matches 116; Conservative
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                18-FEB-2000;
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29-OCT-1999;
30-NOV-1999;
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7 prdsyhlvgisffilglgtllpwnffitaipyfggrlagtnssaetpstnhtsptdtfnf 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newly isolated equilibrative nucleoside transporter protein(s) and gene(s) - used to develop products for treating disorder(s) associated with the transporter(s) and for use with nucleoside
Rat; equilibrative nucleoside transporter; hENT1; hENT2; rENT1; rENT2; coronary; cerebrovascular anoxia; viral infection; cancer.
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Matches 107; Conservative
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N-PSDB; AAV40278.
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30-DEC-1996;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 23, 2002, 17:35:27; search time 3087.27 seconds (without alignments) 6068.071 Million cell updates/sec Run on:

US-08-816-011H-36 1388 1 atggtaataatcaacc Title: Perfect score: Sequence:

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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
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en_gsss.. em_gss_inv:* em_gss_pln:* em_gss_vrt:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BJ119282 BJ119282	AU222343 AU222343	AU201199 AU201199	AU216992 AU216992	AW453425 SWOV3MCAM	AU109268 AU109268	AI082929 SWAMCAC12	AU209436 AU209436	C13829 C13829 Yuji	AU113471 AU113471	AU115402 AU115402	AU114995 AU114995	AL060767 Drosophil	AA406898 MBAFCZ7F0	BI501984 rm07f05.y	AW409482 SWOV3MCAM
SUMMARIES	QI	BJ119282	AU222343	AU201199	AU216992	AW453425	AU109268	AI082929	AU209436	C13829	AU113471	AU115402	AU114995	CNS005TE	AA406898	BI501984	AW409482
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	Score	96.2	86.6	77.6	75.6	75.2	73.8	73.8	70.8	70.2	67.8	57.6	57.4	56.2	54.4	54.4	23
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6.9%; Score 96.2; DB 10; Length 551;

Query Match

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345 9 AU109592 606 9 AA48920 120 II CNSO760F 1201 II CASO760F 274 9 AA48870 228 9 AI784877 229 9 AI739052 350 10 R03450 373 10 C43216 274 9 BB181657 351 9 AU111161 738 II AO842781 759 II AO842781 759 1 AO254298 375 10 C44886 340 9 AU111560 340 9 AU111560 449 9 AW82951 449 9 AW82951 449 9 AW82951 449 9 AW82951 449 9 AW82951 441 10 BF45965 442 9 AA058117 566 9 AW433515 666 9 BB169820	ALIGN 551 190-ca 190-ca 11erry 11erry the C the C the C the C the C to cac.jp	sex="hermaphrodite" tissue_type="whole animal dev_stage="L1" 152 c 94 g 187
408407894949494949494949494949494949494949494	BJ119282 BJ119282 BJ119282 BJ119282. BJ119282. BJ119282. Gaenorhabditis elegans. Caenorhabditis elegans. Capanis, Nemin. Contar, Y., Shin.i,T., The and Sugano, S. Contart: Tadasus Shin.i Intl Yata, Mishima, Shin.i Intl Yata, Mishima, Shin.i Intl Yata, Mishima, Shin.i Corpanism="Caerion/Quality" Contart: Shin.i@genes.nig Incartion/Quality Contart: Tadasus Shin.i Intl Yata Mishima, Shin.i Intl Yata Mishima, Shin.i Intl Yata, Mishima, In	/sex /tis /dev 117 a
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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and Sugano, S.
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                                            911 tcacaagtttcctcgtcttcaatttgttcgctgcgattggatccatagttgcttccaaga 970
                                                                                 TGACCACATTCCTTCAATTCAACGTGTTCGCTTTTATTGGATCAATTGTCGCCGGAAGAA 600
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Caenorhabditis elegans cDNA clone ykl015b04 3', mRNA sequence.
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    Mismatches 173;
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Pred. No. 1.5e-07;
0; Mismatches 259;
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Contact: Yuji Kohara
Gonnem Bilology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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AU222343.1 GI:14860500
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Caenorhabditis elegans
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Best Local Similarity 49.3%;
Matches 255; Conservative
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Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 669)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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  Pred. No. 1.8e-09;
0; Mismatches 173; Indels
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Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
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/dev_stage="L1"
106 c 170 q 151 t
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53.6%;
  Best Local Similarity 53.6
Matches 200; Conservative
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Location/Qualifiers
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AU216992.1 GI:14855149
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Best Local Similarity 51.69
Matches 199; Conservative
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                                                                                                                                               Best Local Similarity
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 332)
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Contact: Yuji Kohara
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
1111, Mishima, Shizuoka 411, Japan
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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/dev_stage="L4"
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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota: Metacoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 710)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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/clone_lib="unpublished oligo-capped cDNA library, stage
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                                                                                                                            114 ATAGTTGACGGTGCGGATAGCTCTGATGAGCACAATGAGCTGATTCCAGAAGATAAGGGA 173
                                                                                                                                                                        67 aatattgictactggctcgtcattcttgttggattcggagttcttctgccatggaatatg 126
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  Length 332;
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Contact: Yull Kohara
Genome Biology Lab.
National Institute of Genetics
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Pred. No. 2.4e-05;
  DB 9;
Score 77.6; DB 9;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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/dev_stage="L4"
103 c 181 q 172 t
                                           0; Mismatches
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us-08-816-011f-36.rst

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ö g δ qq Qγ q ò QQ

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Genome Biology Lab.
National Institute of Genetics
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//dev_stage="molting L3"
//dev_stage="molting L3"
//dev_stage="molting L3"
//note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I: Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameron (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
day 5 in culture. mRNA was isolated from approximately
f000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by Rhase H
and DNA pol I. The library was constructed in the lambda
uni-zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is -1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Wanlewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E 1 (bases 1 to 648)
S Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Science Center, Smith College Department of Biological Science Center, Smith College Northampton, MA, 01063, USA
Tel: 4158853826
Fax: 415885386
Exa: 4158853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW453425
SWOV3MCAM41C06SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM41C06 5',
                                                                                                                                           1189 cactactcaagatttgccgctcagctttccgtttgcactcttatggttggccttctcacc 1248
                                                                                                                                                                                                                               ggtggcctgtggcccgttgttattgagcacttcgtggacaagccaagtatcttataaata 1308
589 ACACTCCCGGTCTTCTTCGAATCCACGTGCTTTTCATCATTGTGGCCCATCGATGAGC 530
                                                                                                                                                                                      TCAAAGGCTCAGGTGGCTGGAATGATGGCTGGATTTTTCCTCATTTCAGGAATCGTCTCA 410
                                                                                                                                                                                                                                                  /db_xref="taxon:6282"
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/clone=lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3)"
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                                                                                   /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Kumba, Cameroons"
                                                                                                                                                                                                                                                                                                          1309 tttatagcattagagtatacttgtta 1334
                                                                                                                                                                                                                                                                                                                                      slustigm@nybc.org).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
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Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y. and Sugano, S.
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                                                                                                                                                                                                 90 tcttgttggattcggagttcttctgccatggaatatgttcattactatcgcccctgagta
                                                                                                                                                                                                                                                                                    208 TGCGCTTCATTTTTTGTCATATCTTGGTCTTGCTTCACAGATACCGAATTTGCTACTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 TCTGATCAACTTATTCGTCCAGATCAAAGGCGATCTCAGACGACGAATTAGCTTTTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 TICTCATATGATCGGTGTATTTTTCTTTATTACCATGACCACAGTGGTGTTATTAAATGC
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                                                                                                                                28 IGATATGGTGTTCGACAAACCTCCCAAAGACAAGTACAATGCTGTTTATTTCATTTTACT
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  DB 9;
Score 75.2; DB 9;
Pred. No. 2.9e-05;
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Unpublished (2000)
Contact: Yuji Kohara
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Unpublished (2001)
Contact: Yuji Kohara
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A1082929 GI:3419555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brugia malayi"
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/dbxref="taxon:6279"
/clone="SWAWGAC12609"
/clone_lib="Brugia malayi adult male cDNA (SAW94NL-BmAM)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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Genes expressed in adult males of Brugia malayi
Genes expressed in adult males of Brugia malayi
Unpublished (1995)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Smith College, Department of Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/tissue_type="whole animal"
/tissue_type="whole animal"
/fore_stage="varied"
/fore compared for the com
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    327
    /organism="Caenorhabditis elegans"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73.8; DB 9;
Pred. No. 6.4e-05;
0; Mismatches 62
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                 Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.3%;
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 495)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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RNase H and DNApol I. The library had 4.6 x 10E6 independent recombinants and average insert size was 800 base pairs. The library was constructed by Noelle Ling. The library is available from Dr. S.A. Williams, email
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National Institute of Genetics
Tata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                             233 t
                                                                                                                                             122 g
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AU209436.1 GI:14845001
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AU113471 and bp mRNA linear EST 19-OCT-2000 AU113471 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk708a4 3', mRNA sequence.
AU113471. GI:10927038
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
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Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
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                                                                                                                                                                                                                                                                                                                                                                                 29 TTANCACATTCCTTCAATTCAACGTGTTTGGCTTCATCGGATCAATCGCCGGGAGNA
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                                      /organism="Caenorhabditis elegans"
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/clone="xk183c7"
/clone="lb="xuji Kohara unpublished cDNA"
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/dev_stage="varied"
) a 107 c 71 g 99 t 4 others
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Contact: Yuji Kohara
                                                                                                                                                                                                                                                                            5.1%; Score 70.2; DB 10;
56.0%; Pred. No. 0.00033;
iive 0; Mismatches 116;
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Fax: 81-559-81-6854
Fax: 81-559-81-6855
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Location/Qualifiers
    Location/Qualifiers
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Best Local Similarity
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Caenorhabditis elegans
Eukaryota; Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Rhabditidae; Peloderinae; Caenorhabditis.
Chases I to 360)
Koharary.'. Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
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                      1...495
/organism="Caenorhabditis elegans"
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/db_xref="taxon:6239"
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51.0%; Pred. No. 0.00024;
ative 0; Mismatches 182;
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Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Far: 81-559-81-6854
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                                                                                                                                                                            /sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
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ykohara@lab.nig.ac.jp.
Location/Qualifiers
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2; Conservative
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    Email:
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AU114995 unpublished oligo-capped cDNA library Caenorhabditis AU114995 unpublished oligo-capped cDNA library Caenorhabditis AU114995
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Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota: Metazoa: Nematoda: Chromadorea: Rhabditida; Rhabditoidea
Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
                                                                                                    1135 catggatacctcagcgctctggcaatgggatacactccaaacgtcgtgccatctcactac 1194
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239 CCTGTTTGGTTTAAGAATGAATGGTGGTTCACTATTGGATGTACCATAATGGCATTTACT 180
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/clone_lib="unpublished oligo-capped cDNA library"
/sex="Hermaphrodite"
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Contact: Yuji Kohara
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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/dev_stage="varied"
67 c 53 q 84 t
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Location/Qualifiers
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Caenorhabditis elegans
Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
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/clone_lib-"unpublished oligo-capped cDNA library"
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Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
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Pred. No. 0.001;
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M. genome@smith.edu."
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/db_xref="taxon:6279"
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Fax: +44 131 670 5450
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L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Osocegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: nb Ws sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                          Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK12X22 of RPCI-98 library from Drosophila melanogaster (fruit AL060767
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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/dev_stage="adult"
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/note="vector: Lambda Uni-Zap XR; Site_1: Eco RI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.
MRNA was prepared from approximately 50 adult females
isolated from the peritoneal cavity of jirds and
converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 5 x 10E6 independent recombinants
and the average insert size is -900bp.The library was
constructed by
library is available from Dr.S.A.Williams, email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA406898 258 bp mRNA linear EST 01-MAY-1997 MBAFCZ7F07T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCZ7F07 5', mRNA sequence.
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Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and Jones
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Onchocercidae; Brugia.
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University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/AFC/MBAFCZ7F07T3.html
Seq primer: T3.
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Unpublished (1996)
Contact: Blaxter ML
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ORIGIN

; Query Match
3.9%; Score 54.4; DB 9; Length 258;
Best Local Similarity 61.1%; Pred. No. 0.53;
Matches 88; Conservative 0; Mismatches 56; Indels 0; Gaps δý qq δλ Q

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X59536 S. cerevisia
M11449 Yeast mitoc
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Waterston, R.
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Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
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Department of Genetics, Washington
St. Louis, Mo 63110, USA, and
Sanger Centre, Hinxton Hall
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Submitted (18-APR-1996) Robert Waterston
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Waterston, R.
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This sequence may not be the entire insert of this clone. be shorter because we only sequence overlapping sections or longer because we provide a small overlap between
                                                                                              neighboring submissions
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chemistry This sequence was finished as follows unless otherwise noted: alregions were double stranded, sequenced with an alternate chemis or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence more than one m13 subclone.

NEIGHBORING COSMID INFORMATION

gene

The 5' cosmid is C46C11, 200 bp overlap;3' cosmid is K02G10, bp overlap. Actual start of this cosmid is at base position CELF16H11; actual end is at 10112 of CELK02G10.

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers /organism="Caenorhabditis elegans" /strain="Bristol N2" /db_xref="taxon:6239" /chromosome="X" .31049 FEATURES

gene CDS

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complement(1239. .2839)
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complement(1239. .1368,1421. .1617,1669. .1878,
1932. .2131,2180. .2466,2516. .2649,2693. .2839))
/gene="F16H11.3"
/note="weak similarity to HNP36 protein"

/codon_start=1

/COCULS_ALL_I
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complement(7137. .7683) /gene="F16H11.4" /note="ceh-1"

gene

complement(join(7137. .7253,7307. .7456,7505. .7573,7621. .7683)) /gene="F16H11.4" CDS

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gene

CDS

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gene

5591 g Q 10124 COUNT BASE CO

Gaps Indels 296; Length 31049; 72.9%; Score 1012; DB 3; 82.0%; Pred. No. 1.9e-259; iive 0; Mismatches 5; Matches 1371; Conservative Similarity Query Match Best Local

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9 2839 ATGCTAATAATCAACCGATCGAACACCTATGCCGTTGAGCAGGAAGCATTTCCAAGAGAC 1 atggtaataatcaaccgatcgaacacctatgccgttgagcaggaagcatttccaagagac

61 aagtacaatattgtctactggctcgtcattcttgttggattcggagttcttctgccatgg 120 2779 AAGTACAATATTGTCTACTGGCTCGTCATTGTTGGATTCGGAGTTCTGCATGG g ò

2719 AATATGTTCATTACTATCGCCCCTGAGGTTTGCAACTAGATAATTTTCACTAATAGAGTT 121 aatatgttcattactatcgccctg--------g δ

----agtattatgtgaattattggttcaaaccggatggcgtggagacatggtattc 2659 146 δ В

2540 257 gaaagaattcatgggatctttgacgattggctcacaacttccaaacgcaagcattaatgt 198 δλ

281 258 tttcaacctgttcctcattattgc-------

TGGATACCTCAGCGCTCTGGCAATGGGATACACTCCAAAGT	AY058347 N Drosophila melanogaster GH12067 full le AY058347 AY058347.1 GI:16182780 FLI_CDNA. fruit fly. M Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Trachea Pterygota; Neoptera; Endopterygota; Dip Muscomorpha; Ephydroidea; Drosophilidae.	Chappe.M., Chavez,C., Dorsett,V., Farfar Munoo,J., Pardea,C., Dorsett,V., Liao,G., Nunoo,J., Pacleb,J., Paragas,V., Park,S. Yu,C., Lewis,S.E., Rubin,G.M. and Celni Direct Submission Submitted (08-OCT-2001) Berkeley Drosop Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA Sequence Submitted by: Berkeley, CA 94720, Tabsequenced as part of a hosequence Clones from Drosophila Gene Coscuence 2000). The sequence accuracy, presence of a pofer and parked and presence of a pofer and presence of a pofer accuracy, presence of a pofer and presence of a pofer accuracy, presence of a po	within 100 kb in the genome. Thus we be reflect accurately this particular cDNA artifacts associated with the generation have not been detected in our initial a priming, priming from contaminating gendue to reverse transcription of unsplicreverse transcriptase errors that result For further information about this sequand relationship to other sequences, plotti; //fruitfly.berkeley.edu. Location/Qualifiers ce	/organism="Drosophism metanoga /Strain="Y; cn bw sp" /db_xref="taxon:7227" /map="26E2_26E2" 12065 /gene="BEST:LD04971" /note="alignment with genomic /db_xref="FLYBASE:FBgn0026585" 3471723 /gene="BEST:LD04971" /note="Longest ORF"
0y 1176 0y 1339 0y 1205 0y 1205 0y 1265 0y 1265 0b 1279 0y 1325	RESULT 3 AY058347 LOCUS DEFINITION ACCESION VERSION KEYWORDS SOUNCE ORGANISM	TITLE JOURNAL	FEATURES	gene
	509 tgattgggaacaacatttgcggattgctgataacggttgtgaaaatcggatgacctatt 568 [2059 CANTIGCACTITICITATION AND ACCARACT ACCACTATOR AND ACCASE AND	1819 TGTTATGATGACGGTTACCACTGGTGGA 888 aaacgatgaaatctacactttgctcaca 111111111111111111111111111111111	1017 tgctctttcattccattcttcttcttctgcaactatcgtgtccagacgcgtgcttatcc 1076
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fan, D., Frise, E., George, R.,
i., Miranda, A., Mungall, C., J.,
i.S., Phouanenavong, S., Wan, K.,
niker, S.
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                                                                                                           tcaccggtggcctgtggcccg 1264
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                                                                                                                                          QLNVPYWQIFKKAAPQLENIFLTFFVTLSVFPAIQSNVHRSDPNFVVGPDYFTLVTCF
ATFNVFAMLGSLTTSWVQWPGPRFLWVPVVLRLAFIPLFVMCNYVPPDSVRSLAVFIE
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This sequence was identified as CDM:10210382 by the submit FOT more information on this record e-mail to fly@celera.ce
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 13429)
Adams, M. and Venter, J.C.
Direct Submission
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Eukaryota: Metagoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metagoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 6467.

(cleniker, S.E., Aghavani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Kearney, L., Kim, S.H., Lee, B. Drosophila on the Mixon K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, D., Snir, E., Nixon K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, D., Snir, E., and Kimmel, B. Sequencing of Drosophila chromosome 2L, region 26F1-26F4

L Unpublished (1997)

L Classes 1 to 64674)

C Cloniker, S.E., Aghavani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Hummasti, S.R., Karra K., Karra K., Karney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mazda, P., Mok, M.S., Moshrefi, A., Moshrefi, M., Nixon, K., Pacleb, J.W., Park, S., Pfeiffer, B., Punch, D., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                archive web site (http://fruitfly.berkeley.edu/sequence-archive.html) or send email to drosophila@genome.lbl.gov.
Library location: 136 81.
This Pl was assembled from the following subclones: 1_b4, 2_b6, 2_d8, 1_b5 (AC003251), 1_c11, 2_e1, 1_f2, 1_g4 (AC003249), 1_g6 (AC003255), 2_c3, 1_e12 (AC003248), 1_h9, 2_e9, 1_a5, 2_e3, 1_e12 (AC003247), 2_h1, 2_b12, 1_a12 (AC003761), 1_g3, 1_g12, 2_e7, 1_c8.
                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Pl DS07773 (D154)) DNA sequence, complete
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Submitted (28-FEB-1998) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
                                                      8219 AGACGGIGCACACCAAAIACCAGACCACIGCCGGAAIGIACGCAGCIGCCAIGCIGAICA 8278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Subclones in Sac from Pl clone DS07773
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1175 acgtcgtgccatctcactactcaagatttgccgctcagctttccgtttgcactcttatgg
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Berkeley, CA 94720
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/clone="P1 DS07773 (D154)"
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DB 3; Length 64674;

Score 90.8;

6.5%;

Query Match

us-08-816-011f-36.rge

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Db 58751 Qy 1115 Db 58691 Qy 1175 Db 58631 Qy 1235 Db 58631 Qy 1235 Db 58571	RESULT 6 AC092230 LOCUS DOCUS DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL COMMENT
Best Local Similarity 45.4%; Pred. No. 3.6e-13; Matches 556; Conservative 0; Mismatches 632; Indels 36; Gaps 5; Qy 47 cattccaagagacaagtacaattgctactggctcgtcattcttgttggattcggag 106	221 cgattggctcacaacttccaaacgcaagcattaatgttttcaacctgttcctcattattg	59393 GGACCACCATGGTGTGTTGTTTAAACGTGTGCAACGGAACAACCA 461 tttatggagttggtgggattttccgcaacctacattggcgctctcttgattggaaaca 1 1 1 1 1 1 1 1 1 1	Db 59096 GGAGCAGCAAAAGAAATCTGATTCTAAGGCCCAGCTGAACGTGCCTTACTGGCAGATCT 59037 Oy 761 tcacaaactgttatgggcaactcttcaatgtttggttctgctttgccgttactctcacaa 820

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCACCATGGTGTGCATTGTGTTGTTAAACGTGTGCAACGGCATCTACCAGAACACACA 39713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39951 GGAGCAGCGAAAAAAAAATCTGATTCTAAGGCCCAGCTGAACGTGCCTTACTGGCAGATCT 40010
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Drosophia melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         107 ttcttctgccatggaatatgttcattactatcgcccc----tgagtattatgtgaatt 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gggtaactcttggaatggcgacttcaatcaattttagcaatgggctatatgaaaactcgg 460
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                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctggtcccctgatctaccgcgtctttgctccggtttgcttcaacatcgtcaacctgacaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39774 ACATCAGCGGCTGCTTCACCACCGCCATGGCCTTGATATGCGGTGAGATCTTCTCGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39891 TCGACACGTACTTTGCGCTGCCGCTGAACAAGTTCTTCCGGCACTACGAGACCATTAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 attggttcaaaccggatggcgtggagacatggtattcgaaagaattcatgggatctttga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcattctcatcctcgtcattgttctggagcccactgaagattccatgtcctggtttttct
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                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                       Length 174376;
                                                                                                                                                                                                                                                                                                                  0; Mismatches 632; Indels
/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/chromosome="2L"
/map="26F-27X"
                                                                                                                                                                                                                                                                         6.5%; Score 90.8; DB 3;
15.4%; Pred. No. 4e-13;
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Matches
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ORIGIN
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EUKATYOTCA METAZOA; Arthropoda; Tracheata; Hexapoda; Insecta;
EUKATYOTCA METAZOA; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Miscomorrha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 259464)

8 Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatidae; P.G., Scherer,S.E., Ill,P.W., Hoskins.R.A., Galle,R.F.,
George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
Brandon,R.C., Rogers,Y.H., Blazely,R.G., Champe,M., Pfeiffer,B.D.,
Wan,K.H., Doyle,C., Baxter,E.G., Hell,G., Walson,C.R., Gabor
Miklos,G.L., Abrill,J.F., Agbayani,A., An,H.J., Basu,A.,
Baxendale,J., Bayraktaroglu,L., Basaley,E.M., Beson,K.Y.,
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Busam,D.A., Butler,H., Caddeu,E., Center,A., Chandra,I.,
Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., Gorrer,S.M.,
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Fleischman,W., Fosler,C., Gabrielian,A.E., Garrell,J.H., Gu,Z.,
Gelbart,W.M., Glasser,K., Houck,J., Hostin,D., Houston,K.A., Howney, M., Harris,M., Methon,P., Celly,Y., Lel,Y., Karpen,G.H., Kavitez,S., Kulp,D., Lin,X., Mattei,B., McIntosh,T.C.,
Li,J., Li,Z., Libang,Y., Lin,X., Lil,X., Mattei,B., McIntosh,T.,
McLedd,M.P., Nelson,D.L., Nelson,D.L., Nelson,D.K., Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear INV 04-OCT-2000 scaffold 142000013386055 section 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40416 AGACGGTGCACACAAATACCAGACCACTGCCGGAATGTACGCAGCTGCCATGCTGATCA 40475
940
tgtctgaaaacgatgaaatctacactttgctcacaagtttcctcgtcttcaatttgttcg
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                                                                                                                                                                                                                                                                                                                                                                                                                           40296 CGGACTCGGTGCGCTCATTGGCCGTATTCATCATCAGAACGATTGGGTGTACTGGGCCATCG
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                                                                                                                                                                                                                                                           1001 ttgccataatcttgcgtgctcttttcattccattcttcttcttctgcaacta----tc
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Drosophila melanogaster genomic
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AE003614 AE002690
AE003614.2 GI:10728613
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Drosophila melanogaster
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KEYWORDS
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ORGANISM
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/note="cli gene product; Nucleotide sequence of the Celera
sequence differs from the published sequence for this
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AASDIDNGSVAGSNLYCCSSASNPLDGGAAVNSSAVAAAAAAYDGKHPYYYYNSWQO

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ENFNNFSTTQQTFDPMVMPPPFT"
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49cne="Cli"
Anote="Nucleotide sequence of the Celera sequence differs from the published sequence for this transcript."
Aproduct="Cr27024"
Adb_xref="FLYBASE:FBBA00009554"
Adb_xref="FLYBASE:FBBA0000320"
complement(<30215. .>38869)
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Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapsleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, K., Zhao, G., Zhao, Q., Zhao, G., Zhao, G., Zhao, G., Zhao, G., Zhao, G., Zhao, G., Zhao, S., Zhu, S., Shu, X., Smith, H.O., Togenome sequence of Drosophila melanogaster Science 287 (5441), 2185-2195 (2000)
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SYSTSHIGADIRULTLDAGGOPTRSMLYFRGSGSALTLLDLMAHQPGCVGYAPLIAYE
SYSTSHIGADIRULTLDAGGOPTRSMLYFRGSGSALTLLDLMAHQPGCVGYAPLIAYE
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FYGLPLERNYTRIQHWHPRGOYFFGSSRWKELSSQSAFEWISEMMVDDIGAVQDVCGG
AMDLWGYRSIQDFNHFSPESFQPIMDKAY"
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ASVDGGPSNSLARSAFYDRFQQQLQQQQQSSQTAVYNLTATIVDVLSAQRSKILAEME
NFEYPRGGAERLTDMTPETNGTPVRSVVVTSWRSGSTFLGDILNSIPGNFYHYEPLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Journal of Adams, Lo. 259464)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Submitted (12-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7297129.
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join(538. .1127,1190. .1366,1421. .1745)
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1. 259464
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Ab_aranism="brosophila melanogaster" / Ab_xref="taxon:7227" / Chromosome="12" / 
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/map="26D7-26D9"
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Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The true left end of clone T04B2 is at 31750 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EMPORTANT This sequence is not the entire insert of clone F44D12. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F44D12 is at 1 in this sequence. The true right end of clone F44D12 is at 6268 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66717 AGACGGTGCACACCAAATACCAGACCACTGCCGGAATGTACGCAGCTGCCATGCTGATCA 66776
                                                                                                                                                                                    CAATGCTGGGCAGTTTAACCACATCGTGGGTGCAATGGCCGGGTCCGAGGTTCCTCTGGG 66536
                                                                                                                                      ctgcgattggatccatagttgcttccaagattcactggccgacaccccgttacctcaaat 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                 ----GTAGGCCCGGACTACTTTACACTGGTCACTTGCTTCGCGACCTTTAAACGTCTTCG
                                                                                                                                                                                                                                                                                                                                                   1055 gtgtccagacgcgtgcttatcctgttttcttttgagtctactgacatttttgtgattggtg
                                                                                                                                                                                                                                                                                                                                                                                             66597 CGGACTCGGTGCGCTCATTGGCCGTATTCATCGAGAACGATTGGGTGTACTGGGCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaattgccatgtcttttcacatggatacctcagcgctctggcaatgggatacactccaa
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                                   tgictgaaaaacgatgaaatctacactttgctcacaagtttcctcgtcttcaatttgttcg
                                                                                                                                                                                                                                           ttgccataatcttgcgtgctcttttcattccattcttcttcttctgcaacta----tc
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
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2 (bases 1 to 31853)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66777 CGGCATCTTCTCCGGAGTGCTGT
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Z68298.1 GI:1130621
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VERSION
KEYWORDS
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REMARK
REFERENCE
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TITLE
JOURNAL
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TITLE
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/map="26E1-26E2"
/db_xref="FLYBASE:FBan0009595"
/db_xref="FLYBASE:FBgn0031829"
/db_xref="FLYBASE:FBgn0031829"
/gene="CG9595"
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                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65721 GACCAAACAACACCGTGGCCACGGAAGTGAGTTACCGCACCCATTTCATGCAAAAATATGG 65780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65601 CAGCGCCAAAAGATACCTTATCGTGTTTCTTATATTCCTGCTGCACGGCGTGGGCA 65660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65841 GCGGCGACCTGACCACCCGAATCGTCTACAGCATCATCTTCGAAATGGTCATTCTGCTGG 65900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65901 TTACCATTATTTTGGCCATGCTCG-----ACTCCTCGCAGTGGCCGGCGTCTTCTTCT 65954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65955 GGACCACCATGGTGTGCATTGTGTTAAACGTGTGCAACGGCATCTACCAGAACACCA 66014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66192 TCGACACGTACTTTGCGCTGCCGCTGAACAAGTTCTTCCGGCACTACGAGACCATTAGCC 66251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGCAGCGAAAAGAAATCTGATTCTAAGGCCCAGCTGAACGTGCCTTACTGGCAGATCT 66311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAAGAAAGCAGCGCCCCAACTATTCAACATCTTCCTCACGTTTTTGGTCACGTTGTCGG 66371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 ttcttctgccatggaatatgttcattactatcgcccc----tgagtattatgtgaatt 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgattggctcacaacttccaaacgcaagcattaatgttttcaacctgttcctcattattg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctggtcccctgatctaccgcgtctttgctccggtttgcttcaacatcgtcaacctgacaa 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 catttccaagagacaagtacaatattgtctactggctcgtcattcttgttggattcggag 106
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 attggttcaaaccggatggcgtggagacatggtattcgaaagaattcatgggatctttga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tttatggagttggtggcgattttccgcacacctacattggcgctctcttgattggaaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66075 ACATCAGCGGCTGCTTCACCACCGCCATGGCCTTGATATGCGGTGAGATCTTCTCGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 agcctaaacttgttgcaatcgtctatttcggcatatcgttggtgatccttctggtgtgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcattctcatcctcgtcattgttctggagcccactgaagattccatgtcctggtttttct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcacaaactgttatgggcaactcttcaatgtttggttctgctttgccgttactctcacaa
                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                       Length 259464
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                         8; DB 3;
4.le-13;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 632;
                                                                                                                                                 /note="CG9595 gene product"/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                         Score 90.8;
                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                         6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                     45.48;
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 45.49
Matches 556; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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complement(15660. .15989)
/gene="F44D12.3"
/note="contains similarity to Pfam domain: PF00635 (MSP
/Major sperm protein) domain), Score=111.7,
E-value=4.7e-30, N=1
CDNA EST yk57e8.3 comes from this gene; cDNA EST yk102a1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MQTILIQLIVLFTLFHEVNTLVTCSRCEFGNEECNFSRSTCRGD
FCYHAQYFYGNEMMPTIQKGCVIGEVAPEGCRVNHHGNVMCFCSDADYCNANYTSLAD
TATTILPVQTCQPEKVNNMPKPRWTKPCAANYCTFIEAKTQTEVNSANYTWSTKDCNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENEFDFFPTLTVFNFYPGTCVWLNYGGQPDTHACYGSDSLDTTLVFDVTTATTECHVD
YFNPRLPYVKSGSSCIGQFCFISATSRGEVFRGCVNSVTVEGATPLKIGYTRAYTGLE
QWICDQSYCNADLKSAELSWPPELYLYRNISNLREFNVFYIDSARSSSSIFLAIPIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="wirkHmQQEEEGSPLSYFQYLHVEYNICNGRKWGQTTLKMNEELA
BRSSYVGNOSQTGLYPPRDTWGRKESSPPDRWILVYIIFTMHGMGMLMSWNMFITIAPQ
YYHDYWFNNTNYQDSFMSIIGYGDINVGIMILNTIVVMV"
COMplement(15660. .15989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA EST yk102a1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNT EST YAI2225. Comes from this gene; CDNA EST YAI3225. Comes from this gene; CDNA EST YAI3122. S comes from this gene; CDNA EST YAI3122. Comes from this gene; CDNA EST YAI3140. Comes from this gene; CDNA EST YAI3061. S comes from this gene; CDNA EST YAI3061. S comes from this gene; CDNA EST YAI3965. Comes from this gene; CDNA EST YAI3961. S comes from this gene; CDNA EST YAI312.3 comes from this gene; CDNA EST YAI312.3 comes from this gene; CDNA EST YAI3061.3 comes from this gene; CDNA EST YAI30610.3 comes from this gene; CDNA EST YAI30610.3 comes from this gene; CDNA EST YAI30611.5 comes from this gene; CDNA E
complement(join(7556. .7673,7717. .7832,8096. .8296,8340. .8510,8562. .8718,8944. .9111,9541. .9638))
/gene="F44D12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yk303a11.3 comes from this gene
cDNA EST yk303a11.5 comes from this gene; cDNA EST
yk302c7.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(12326. .12380,12427. .12481,12574. .12895)
/gene="F44b12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(12326. 12380,12427. 12481,12574. 12895)
/gene="F44D12.9"
                                                                                                                                     comes from this
                                                                                                                            /note="CDNA EST yk169e12.3 comes from thi
CDNA EST yk367d4.3 comes from this gene
CDNA EST yk367d4.5 comes from this gene
CDNA EST yk55319.3 comes from this gene
CDNA EST yk55319.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comes from this gene
cDNA EST yk57e8.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q20392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q20396"
                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA92598.2"
/db_xref="G1:5824507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA92605.1"
/db_xref="G1:3877156"
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                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comes
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                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(3277. 3413,3774. 3951,3994. 4239,4318. 4603,
4647. 4894,4945. 5180,5225. 5395,5449. 5759,5805. 6053,
6100. 6802,6846. 7020,7211. 7306,7357. 7425)
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AHGSPFDNYLKLDHIMMYNDISYTDMDERSYMGMLSNCHHIHLVIRRRNCNKISDV
CLPLNYGVGLELSNGYFINSCEPNGASCLAPGGRVYHVMHTPVYDAKHAEMLIKN
SREPLYIGILGSTRRGDHNGKDKHRQTIFSRRFSRNGGSDKERTVYAKANIDRSNDQV
LLRQGSLRMPQASPASMSPLVRYGSLRAPTYSSSIDHTKLMLDALDKRFNAKSTAHSE
                         The end of this sequence (31750. .31853) overlaps with the start of sequence \mathbf{Z}68299.
                                                                                                                                                                                                                                                                                       the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHPPVYPTIRDDSMSSVMSSSNSIRLPSTSFSNQYPNNSTCSLTGGSGVPPRHCISKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSDFSISTTGSAMHSYAEGRSNKKYHLPRGNHHSESLLVNRSSQPRLVEVPRSDVKLC
GGNAIGILAEKSIGSDLLEGDLILSIDGNCVRNTTLECAMNTLSADNSELFGLLVQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEKEIREVEAKWMEKVRKASEERDDIGKKIDEFEEKIDSLQIQV
HRSETYKMEIEEBANKRLRLQYEALQRDYEETWQERSIVLEENSRQNEERDRLQKEIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKEDSEEVAALKOKLENTRRLLKVNMEETAQANARKEAAIARLTEAEONGARITEERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSSSTAAPTALWSPSSVNEKDLVFAGTNIEGVPVYVPKSTIFSTPTSPVTRLIRQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQKRTMSQISSHRGGWDGRSFSSNTTTSDARPYSMHFTPTSSTIMEGKPHRRSAVYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDRLNRLRLGADGDSFFLRVNIDRSMENKDELDLKCGDVVFVDKTMLMGKTGRWRAWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDKEGRQREHGAIPSSTTVYQAIRANRYANPFPKKAYEWVEKLDTKVKRPVLLFGAVV
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IMDITAQGLHCVLQVDQSAIDRLKRCRMFPILVKIRFKSVKQLKDVNEHICGEKISSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAKQLIEKDLKIEKDLDGSVTLVVPSHNNVSFMMTHAVLQLKKIIEDEQKKIVWVQRK
                                                                                                                            For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=F44D12
IMPORTANT: This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note-"Similarity to Mouse Tight junction protein 20-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(3277. 3413,3774. 3951,3994. 4239,4318. 4603,
4647. 4894,4945. 5180,5225. 5395,5449. 5759,5805.
6100. 6802,6846. 7020,7211. 7306,7357. 7425)
79ene-"R44D12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(7556. .7673,7717. .7832,8096. .8296,
8340. .8510,8562. .8718,8944. .9111,9541. .9638))
/gene="P44D12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE), contains similarity to Pfam domain:
(PDZ domain (Also known as DHR or GLGF).),
.0, E-value=5.5e-07, N=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA EST Yk16d12.5 comes from this gene CDNA EST Yk16d12.5 comes from this gene CDNA EST Yk126d.5 comes from this gene CDNA EST Yk129c3.3 comes from this gene CDNA EST Yk129c3.5 comes from this gene CDNA EST Yk129c3.5 comes from this gene CDNA EST Yk360112.5 comes from this gene CDNA EST Yk360112.5 comes from this gene CDNA EST Yk35d5.5 comes from this gene CDNA EST Yk32d9.3 comes from this gene CDNA EST Yk139d.5 comes from this gene CDNA EST Yk139d.5 comes from this gene CDNA EST Yk139d.5 comes from this gene CDNA EST Yk219d.5 comes from this gene CDNA EST Yk216f.5 comes from this gene CDNA EST Yk36f10.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SW: ZO1_MOUSE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="F44D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score=35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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In may be shorter because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true right end of clone C47A4 is at 40664 in this sequence. The true left end of clone F52D4 is at 101 in this sequence. The true tright end of clone F56F12 is at 9819 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence 280218.

The end of this sequence (40564. .40664) overlaps with the start of sequence 282273.

For a graphical representation of this sequence and its analysis see: . http://wormbase.sanger.ac.uk/perl/acc/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB62792.1"
/db_xref="G1:6562350"
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KLYLIRKYIGVSQMEFDQKYTDEDIDDLFERECWLKTNCATWKAERDAAEQEKMAQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVŠLIIVMAMNASNGLYQNSFFGMAADFPAKYSNAVVIGTNICGTFTSVLAĪVATLAF
STQAETVALIYFGISLLILFVCLVSWWFCKKMCWLQCICVFLVYFVSLSVFPTVLAGF
QPGYTVFPNDVYAGIAVFLNFNFFAAVGNVAATFVTFPGPRLLIVPCVIRLLFIPFFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q9U3L8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEDKGRIVFWIILLNGIGVLLPWNMFITIAPQYYVDYWFTVNGTATHYADSFQSAMGV
VAQVPNLIVAIINVLNLIRGPLLYRVLAPLAFNSLLIVIILLALVIFQQPSDQARNWFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSNYLPHSRTMGVLFTNEWIFFEGNTLLAFTSGYFSSLGMMYTPRVCPPEYSKLAGQV
gat gyvygytracysgervathammannel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(28627. .28707,28755. .28832,28884. .29024,
29070. .29267,29338. .29466,29527. .29850))
/gene="C47A4.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .28832,28884. .29024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(15737. 15769,15884. 16078,16580. 16814,17751. 11
18821. 18923,18970. 19055,19306. 19502,20056. 20176)
/gene="C47A4.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(15737. .15769,15884. .16078,16580. .16814,17751. .1
18821. .18923,18970. .19055,19306. .19502,20056. .20176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="C47A4.2"
/note="contains similarity to Pfam domain: PF01733
(Nucleoside transporter), Score=142.5, E-value=2.4e-39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Ser/Thr protein phosphatase), Score=476.0, E-value=1e-139, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(28627, .28707,28755, .28832, 29070, .29267,29338, .29466,29527, .29850))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4254))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3973,4192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB62793.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(3491.
/gene="C47A4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="C47A4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="C47A4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(15737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .40664
                                                                                                                                                                                                                                                                                                                                                                                                   name=C47A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12947 GGTTTCATGATGCTTCGAGTTGTGGTTCCTCTCATTGTGAACTGCATTTTGATTGGGGTC 13006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13127 TACGGAATCGTCGCCGATTTTCCGGATAACTACATTAACTCTTTGGTTATTGGAAACAAT 13186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 ggtcccctgatctaccgcgtctttgctccggtttgcttcaacatcgtcaacctgacaatc 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 attotoatcotogtcattgttctggagcccactgaagattccatgtcctggtttttctgg 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtaactcttggaatggcgacttcaatcaattttagcaatgggctatatgaaaactcggtt 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tatggagttggtggcgattttccgcacacctacattggcgctctcttgattggaaacaac 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                        CDNA EST Yk233c12.5 comes from this gene; cDNA EST Yk232q4.3 comes from this gene conda EST yk232q4.5 comes from this gene; cDNA EST yk232q9.5 comes from this gene; cDNA EST comes from this gene; cDNA EST pk232f9.5 comes from this gene; cDNA EST cDNA EST yk232f9.5 comes from this gene; cDNA EST
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cDNA EST yk302c7.5 comes from this gene; cDNA EST
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                                                                                                                                                                                                                                                                                                                                                                                                      8; DB 3; Length 31853;
1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                    CDNA EST yk262a3.5 comes from this gene;
yk233c12.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 117; Indels
                                                             cDNA EST yk278d6.5 comes from this gene;
                                                                                                                             dene;
                                                                                          yk264e2.3 comes from this gene
cDNA EST yk264e2.5 comes from this
yk262a3.3 comes from this gene
                                comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 13187 TTGTGTGGAGTTTTTACTTCAGTATTGAGTAT 13218
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Mortimore, B.J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   6.18;
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                                /k278d6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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AUTHORS
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KEYWORDS
SOURCE
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TITLE

CEC47A4

RESULT LOCUS

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REMARK

COMMENT

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.18037,

us-08-816-011f-36.rge

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EKEKEKPKKKEKEKEWSGEDASIKFKELRFNQSEGGVRRDTEASCPNRCKMQSHSSRN
RHTDYKCYDHNRITYQMCKDDYINGSKINVPHFTPSITYOQLPKMDSVDAVEEFWRVY
FHEGCQTVHIIARPEELTHYADIDKLFCQESGAMLYANGFFVNTRKVEKKENAKADMFV
VELLPEGCSTAVHORYVENGYKLHTYWKPLFCPDRFCAQIRAAHOIAKNENSYPTYLASVNG
SGRNAALLILAVVEDQLTRGKEPKISEIVRTIREQRPQSVDSYIQYVSLYMATNWLIK
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LISARIDISHWYSKIEAIYEBLOSLLHFLYFLRSASINYDTQNRELMWHAFRDVILLTYP
FIERARQRIVKQKLDRRFYSSIGSSDIECVVCDKPSVIPWYGQKCGHVACYTCIATS
RNMTCPLCSENAEPMBFLAKKLKNPILIE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SW:PAFI_RAT), contains similarity to Pfam domain: PF00097 (Linc finger, C3HC4 type (RING finger)), Score=16.2, E-value=0.00035, N=1
                                                                                                                                                                                                                                                                                     neighbouring submissions.
The true left end of clone 2K809 is at 1 in this sequence. The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The end of this sequence (25461. .25560) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPNKNGVGKKSPSTSKSSNNNKRREPESRYEEKTAVHGGKTKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKTVVHGGKTKNVVAKKVPSKASVIVDKKASTTETTVPITVKKSMLSISTAYDRTVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MIHHFRYHQKRNILPNNTLHCTLPHYHYSFSVLFLSDTSFYLIF
                                                                                                                                                                                                                                                                                                                                                                                                       The true left end of clone ZK792 is at 25461 in this sequence. The start of this sequence (1. .113) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is NOT necessarily the entire insert of
                                             Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a daye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone ZK809. It may be shorter because we only sequence overlapping sections
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                  y be shorter because we only sequence overlapping sections or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(3252. .3612,3660. .3835,4567. .4606,5066. .5406)
/gene="ZK809.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similarity to Rat peroxisome assembly factor-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(1372. .1376,1431. .2001,2054. .2551,2599. .2803,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity to Pfam domain: PF00102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(1372...1376,1431...2001,2054...2551,2599...2847...2854)
2847...2854)
/gene="zk809.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(3252. 3612,3660. 3835,4567. 4606,5066.
/gene="zk809.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score=35.2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA EST yk560a11.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Protein-tyrosine phosphatase), Score=35
E-value=2.3e-13, N=1
cDNA EST yk365g6.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKLPSGHEVVSKIKKFNEKATRSLPGSMMKTPTEEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .25560
Coganism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="IV"
                                                                                                                                                                                                                                                                                                                                                right end of clone ZK809 is at 15121 in sequence Z68302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA92641.2"
/db_xref="G1:5824906"
/db_xref="SPTREMBL:023602"
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/db_xref="G1:3881798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2847. .2854)
/gene="ZK809.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="ZK809"
                              available information,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence Z68302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                name=ZK809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                         LLLAYKVKFPCNFFLLRGNHECEFVNKTYGFYEECQKRYQSVRXAARQOVFNMLELT
LLLAYKILCHGUSPLMTKEFTLDTLRKIERFTEGKEGLVADLLMADPISGLGGFMN
NORGAGCGFGRDSVLNLCSFEQLDLVCRAHQVVQDGYEFFAGRKLVTIFSAPHYCGQF
DNCAAFMSCDEKLQCSFEILRPTTGRLEIRERPLLKDSTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MADKSAFVPVDAIGNHKNTDLDVDIDDELFGKKPPKTAEAPKPA
PPPPAPAPAAAPSTGKYQYKKSSTYQKSYAK"
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                           /translation="MQNNVVDSIIIDVLSASTHEKPLCKVITTEFVLKLLDLALGVFK
AQKPMVEVNAPIKVCGDIHGQFPDLLRLFHRGGWPPTANYLFLGDYVDRGRFSIETIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INV 11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein like; Peroxisome assembly factor
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Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17878 TATTGGAACAATATTTGTGGAACATTCACTAGTGTCTTGGCAATTGTCGCAACTTGGC 17937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17938 ATTCTCAACACAAGCTGAAACTGTTGCACTTATTTATTTTGGAATATCACTTCTTATTCT 17997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 tgaaaactcggtttatggagttggtggcgatttccgcacacctacattggcgctctctt 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570 tctgaatgatgagcctaaacttgttgcaatcgtctatttcggcatatcgttggtgatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17818 CCAAAACTCATTTTCGGAATGGCTGCAGATTTTCCCGCAAAATACTCGAACGCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 gattggaaacaacatttgcggattgctgataacggttgtgaaaatcggagtgacctattt
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Caenorhabditis elegans cosmid ZK809, complete sequence.
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.1%; Score 71.2; DB 3; 53.6%; Pred. No. 6.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128;
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                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q9U3L6"
/db_xref="SPTREMBL:Q9U3L7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6544 q 13766
                                                                                                                                                                                                                                                                                                                                            /protein_id="CAB62795.1"
/db_xref="G1:6562353"
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/gene="C47A4.5"
33294. .33521
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/gene="C47A4.5"
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Caenorhabditis elegans
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                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:Q23597"
/translation="MGNQYVKPERTGNSPYTRSGVPPPALVKTGDKPLHRVNDRMSLE
LHMADERVRAAGLSPAEREWRKKWVHDQHLHADEPVVVDAVHRQLNPIRTAYRLPWDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(12918. .13232,13332. .13978,14028. .14122,
14201. .14367,14519. .14680))
/gene="ZK809.4"
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llarity 52.0%; Pred. No. 7.5e-08;
Conservative 0; Mismatches 147; Indels 0;
                                                                              CDNA EST yk665g12.5 comes from this gene"
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpow virus
Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
166494.1 GI:2724471
                                                                                                                                                                  /protein_id="CAA92637.1"
/db_xref="GI:3881795"
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/protein_id="CAA92642.1"
/db_xref="G1:3881800"
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TRMYQLGEKVGDLPKGSSLEILRKNPPIEY"
Join(11625. 11731,11785. 11887,11940. 12056,12122. 12232,
12286. 12419,12469. 12529)
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//gene="zk809.3"
//note="predicted using Genefinder
cDNA EST yk78b3.3 comes from this gene; cDNA EST yk78g8.3
comes from this gene
cDNA EST yk105h6.3 comes from this gene; cDNA EST yk78b3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comes from this gene
cDNA EST yk78g8.5 comes from this gene; cDNA EST yk105h6.5
comes from this gene
complement(join(10131. 10337,10438. 10717,10774. 10870, 10916. 11035,11085. 11127))
/gene="ZK809.2"
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VYQKGMDFCVDMLNDNKWYHIFPEGKVCTLESEPLRFKWGIGRLVMDAKTDPVILPVW
                                                                                                                                                    complement(join(10131. 10337,10438. 10717,10774. 10870, 10916. 11035,11085. 11127))
/gene="zk809.2"
/note="contains similarity to Pfam domain: PF01553
/Acyltransferase), Score=144.3, E-value=7e-40, N=1
cDNA EST yk576b1.3 comes from this gene
cDNA EST yk576b1.5 comes from this gene
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Submitted (199-Aug-1996) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CBIO 15A, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
On Sep 24, 1998 this sequence version replaced gi:1515146.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
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                                                                                                                                                Gaps
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                           4.9%; Score 68; DB 6; Length 7218; ilarity 4.2%; Pred. No. 3.8e-07; Conservative 234; Mismatches 149; Indels
                                                368 others
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                               /organism="unknown"
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Location/Qualifiers
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dye primer and dye terminator reaction, from distinct subclones.

Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone K09A9.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone K09A9 is at 35278 in sequence 279596.

The true right end of clone K09A9 is at 240A1 in this sequence. The true left end of clone K09E9 is at 104 in this sequence. The true right end of clone C02C6 is at 104 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence 279596.

The end of this sequence (33914, .34017) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 279602.
For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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or on a single strand with both
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/chromosome="X"
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/db_xref="GI:3878424"
/db_xref="SWISS-PROT:Q93873"
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REST EMBL: M89294

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REST YK68h5. 5 CO

REST YK68h5. 5 CO

REST YK70h1. 3 CO

REST YK48f93. 5 CO

REST YK40f91. 5 CO

REST YK20910. 5 CO

REST YK20910. 5 CO

REST YK506b9. 3 CO

REST YK506c9. 5 CO

REST YK506c9. 5 CO

REST YK506c9. 5 CO

REST YK506c9. 5 CO

REST YK606g8. 3 CO

REST YK506c9. 5 CO

REST YK506c9. 5 CO

REST YK606g8. 3 CO

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                                                                                                                                                                                                                                                                   gene
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join(13620. 13793,13874. 14074,14437. 14532,14631. 14697,
14741. 14641,14689. 15017,15106. 15351,15397. 15632,
15939. 16205,16346. 16496)

/gene="R09A9.4"
join(13620. 13793,13874. 14074,14437. 14532,14631. 14697,
15939. 16205,16346. 15017,15106. 15351,15397. 15632,
14741. 146441,14889. 15017,15106. 15351,15397. 15632,
/gene="R09A9.4"
/gene="R09A9.4"
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FGPQHPAAHGVLRLVLKLEGEVIIKAIPHIGLLHRATEKLIEHKTYTQALPYFDRLDY
VSMMCNEQAMSLAVEKLLGIDIPTRAKYIRTLMGELTRIQNHIMGITTHALDVGAMTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="Cab01885.1"
/db_xref="G1:3878423"
/db_xref="SPTREMBL:093875"
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ODCINSLKSSCCKNSDHLLPHMAVHNHPPILYHDRKSILCTRCMYTPVKRFLTHTKF
                                                                                                                                                                                                         LEDMLTENRIWKARTIDIGLVSAADALNWGFSGVWVRGSGIKQDVRKTEPYDAYADME
FDVPIGTKGDCYDRYLCRIEEMRQSLNIVHQCLNKMPAGEIKVDDHKVVPPKRAEMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"SPTREMBL:093871"
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GTLAPWINMLITIOSYPESYKMLANSTIDMDTGKVTGDPTVYSNFGSFQTIASQVPN
LLLINLLNIFIVVKGGLAGRIIVGLSIVAVCYITTMIFIVVETSTWLTGFFTLTITII
                                                                                                                                                                     FFWMFEEREKLFEFSERVSGARMHANYVRPGGVAWDLPIGLMDDIYDWAIKFPERIDE
                                                                                                                                                                                                                                                                                              NMESLIHHFKFFTEGFQVPPGATYVPIEAPKGEFGVYLVADGTGKPYRCFIRAPGFAH
'translation="MLGRKIAGTCLRANVPSVAATSSTPATQTRNSHTIWYPDAKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Similarity to Yeast ubiquitin carboxyl-terminal hydrolase (SW:UBPD_YEAST), contains similarity to Pfam domain: PF00442 (Ubiquitin carboxyl-terminal hydrolases family 2), Score=55.1, E-value=4,9e-13,N=1; PF00443 (Ubiquitin carboxyl-terminal hydrolase family 2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"predicted using Genefinder
/note-"predicted using Genefinder
contains similarity to Pfam domain: PF01733 (Nucleoside
transporter), Score=501.6, E-value=1.9e-147, N=1
cDNA EST ENEL:NY9812 comes from this gene
cDNA EST yk106d4.3 comes from this gene
cDNA EST yk78h6.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA EST EMBL: 214811 comes from this gene
CDNA EST yk527f6.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this gene
this gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yk111h7.3 comes from this gene
yk11699.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-value=0.00029, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comes from to comes from the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:3878420"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yk106d4.5
yk111h7.5
yk11699.5
yk143f7.5
yk183c7.5
yk183c7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yk4888.3 c
yk4888.5 c
yk247h5.3 c
yk247h5.5 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yk78h6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score=12.8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONA EST CON
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gene

CDS

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complement(join(27534. .27696,27760. .27878,28371. .28615,28762. .28867)
28762. .28867)
/gene="K0949.2"
/note="Simiality to Rat RAS-related protein RAB-14
(SW:RB14_RAT). contains similarity to Pfam domain: PF00071
(Ras family). Score=319.6, E-value=1.2e-92, N-1
cDNA EST ykl1555.3 comes from this gene
cDNA EST ykl7915.3 comes from this gene
cDNA EST yk47915.3 comes from this gene
cDNA EST yk47915.3 comes from this gene
cDNA EST yk47915.5 comes from this gene
cDNA EST yk47915.5 comes from this gene
cDNA EST yk47915.5 comes from this gene
cDNA EST yk291f2.5 comes from this gene
cDNA EST yk291f2.5 comes from this gene
cDNA EST yk59411.5 comes from this gene
                               AYESIALITLUFCEISFHILKKQRFYQFYSTRAERQRAKNEEAADNEGKMANYIATFK
EAFPQLINVFLVFFVTLSIFPGVMMYVKDEKKGGTYDFPLPQNYFMDVTTFLQFNVFA
FIGSIVAGRKQWPAPNKLMIPVYLRLLYIPFFIFCNYLPETRTLPVFFESTWLFIIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                  ASMSFGSGYFSGLSMMYTSKTVDPSKAQVAGMMAGFFLISGIVSGLIFTMVIKFVVTA
VLNGANGVYQNSIFGLASELPFKYTNAVIIGNNLCGTFVTLLSMSTKAVTRNILDRSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INV 22-MAY-2000
                                                                                                                                                                                                 complement(join(27534. .27696,27760. .27878,28371. .28615,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R-CG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclophilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCTTCTGCAACTACCTCCCTGAGACCCGCACACTCCCGGTCTTCTTCGAATCCACGTG 25379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGATGTACACTTCAAAGACTGTCGATCCATCAAAGGCTCAGGTGGCTGGAATGATGGC 25499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATTTTTCCTCATTTCAGGAATCGTCTCAGGTCTCATTTTCACTATGGTCATCAAG-- 25557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gccgacaccccgttacctcaaatttgccataatcttgcgtgctcttttcattccattctt 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cattittgtgattggtggaattgccatgtctttttcacatggatacctcagcgctctggc 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aatgggatacactccaaacgtcgtgccatctcactactcaagatttgccgctcagctttc 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-acetylglucosamine-1-phosphate transferase; protein kinase; R-Grebel, R-FA3 repeat; repl1; rep20; rifin; RNA-binding protein; stevoz; T-complex protein 1 epsilon subunit; telomere; var. malaria parasite P. falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cttcttctgcaactatcgtgtccagacgcgtgcttatcctgttttctttgagtctactga 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgtttgcactcttatggttggccttctcaccggtggcctgtggcccgttgttattgagca 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum MAL3P7, Complete sequence.
AL034559 AL008974 AL008975 AL008981 AL008983 AL0089015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169
AL010187 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888
AL139179 298556 298557 298558
AL034559,4 GI:8022273
AL034559,4 GI:8022073
AL034559,4 GI:8022073
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AL034569,4 GI:8022073
AL034569,4 GI:802071-1046 Protein; HesB-like domain
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1 (bases 1 to 253305)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65.8; DB 3; Length 3
Pred. No. 1.7e-06;
); Mismatches 172; Indels
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/gene="K09A9.2"
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51.0%;
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indicate splicing" house donor at 3'
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/translation="Makthundpepinnyynkeennpiicesdekertkiystnh

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NYTNIHNNNNNNNNNNSNEYSYSKKNENNNLINNINNAYORPRIKPIGESEBNIYS

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YNETIRDLIGKERNKTLEVOEDVARVKNONCIPULEFTIINEKKCRNIKVLIMBFLEV

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KNUSSKOLYKOLYKOFEKQPLILENINLEDTENNINNSSWELKODITWANDLOKEYDTLLGKY

KNUSSKOLYKOLYKOFEKQPLILENINLEDTENNINNYVINSKDVNDNNKSLLEENIFKHNENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PFC0860w" (MAL3P)-1), Kinesin-related protein, len: 1200 aa; similarity: to kinesin-related protein. 1200 aa; similarity: to kinesin-related protein. Demelangaster kinesin-like protein 674 (Rr. P91945) BLAST Score: 664, sum (21) = 1.9e-67; 28% identity in 707 aa overlap, predicted using hexExon, Pfam: match to PF00225 kinesin, Kinesin motor domain Score 311.54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEGKSESHNKNNKDDIEDNDKDTIKDIHNNNNSSDNNDDEYQSANSPVESDIVKKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKIPINMETKKKRTMNGTKDPIHKTPYDINIVGILNKEDVSNKSNDYNTNKNIEKNNY
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                         Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J. E., Whitehead, S., Woodward, J.R., Newbold, C. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oliver, K., Bowman, S., Harris, D., Lawson, D., Quail, M. and Barrell, B. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 14, 201 this sequence version replaced gi:2982540 gi:2982541 gi:2982541 gi:2982541 gi:2982541 gi:2982554 gi:2894453 gi:2894464 gi:2982556 gi:2982558 gi:2982558 gi:2982558 gi:2982563 gi:2982563 gi:2982564 gi:2982569 gi:2982569 gi:2982569 gi:29825959 gi:2982599496 gi:2982579 gi:2982599 gi:2984589 gi:2982539 gi:2982539 gi:2984380 gi:2982592. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.

Location/Qualifiers

1. 253305
/organism="Plasmodium falciparum"
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                                                                                                                                                                                                                                                                                                          The complete nucleotide sequence of chromosome 3 of Plasmodium
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/protein_id="CAB39023.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFC0860w, MAL3P7.1"
458. .4060
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Lawson, D., Bowman, S. and Barrell, B.
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                                                                                                                                                                                                                                                                                                                                                                          Nature 400 (6744), 532-538 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="MAL3P7"
458. .4060
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                                AUTHORS
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CDS

FEATURES

COMMENT

Join (3457. 5577,5689. 5787,5923. 6077,6189. 6743)
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Direct Submission Submitted (29-OCT-2000) USDA Forest Service, 359 Main Road, Delaware, OH 43015, USA Location/Qualifiers

Garner, K.J. and Valaitis, A.P.

AUTHORS JOURNAL

FEATURES

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gene

CDS

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DENNTTMGIYKYGEKVDSNNYISEDEININNQLNSEGYLKNDIYMNELNDNYNNDFDD
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LNVKRHMKHIDEDIMYEDMSNSNNFVIFGCFKKVYNQLSGDNNLNISDGIQSVCEDSN
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KMRPYKIYTFSSIFNNDLNILYFFKYFFCNNKDNLKGSLQTIAYGQNYEINNKFINKK
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RVYEQDIQLYKGEGIYTNDENQFDDYIDKYSLYDLRGKEDRKQLRENMLKGRHGKNNY
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AF317619 3065 bp mRNA linear INV 02-NOV-2001
Lymantria dispar aminopeptidase N3 (APN3) mRNA, complete cds.
AF317619
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                                                           78912 TAATTAATCTATGTTTTTTTTTTTTTTTTTAAAGTATGAATATAATATAAAA 78971
                                            1266 tgttattgagcacttcgtggacaagccaagtatcttataaatatttatagcattagagta 1325
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 3; DB 3;
0.13;
Score 47.8; DB Pred. No. 0.13; 0; Mismatches
                      0
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 3.4%;
                       Conservative
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           Local Similarity
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                      16;
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Eŭkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Lepidoptera; Glossata; Ditrysia; Noctucidea; Lymantridae; Lymantria.

1 (bases 1 to 3065)
Garner, K.J. and Valaitis, A.P.
Cloning and characterization of four distinct gypsy moth midgut aminopeptidase. Nenzymes related to the Bacillus thuringiensis

REFERENCE AUTHORS

TITLE

(bases 1 to 3065)

CrylAc receptor Unpublished 2 (bases 1 to 3

JOURNAL REFERENCE

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GLKITTRELDDYLSIQYHEMGGGYLMKNDHIALPDFPSGAMENNGWNYREAYLLYDON
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VGARNFRSALRYYLREHAYEIGTPADMYAAFRRVAAEDFQFPRDY PNIDVGAVEDWY
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PVGLDVSEPPSTDSYYELLKINLSSAIPIGNYTLTVRYTGVINENPIDRGFYMGYYFL
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STTRVQEIFYPTPIISAYLVAFHVSDFVETELTSTPAKPFKIISRPGVTDQHDYAADI
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Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of known genetic parameters within the mhc
Patent: WO 0200932-A 12 03-JAN-2002;
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Transmembrane potassium ion channel protein; inward potassium flux; ss; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; CORK.
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                                                            New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions \,\cdot\,

    241 aacgcaagcattaatgttttcaacctgttcctcattattgctggtcccctgatctaccgc 300
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100.0%; Pred. No. 0;
Live 0; Mismatches
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                                                                                             Example 14; Fig 9; 131pp; English
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Best Local Similarity 100.
Matches 1388; Conservative
                             WPI; 2001-536570/59.
                                         P-PSDB; AAU07630
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potassium dependence; Saccharomyces cerevisiae; potassium-agonist;
potassium-antagonist; drug screening; nematocide; anthelminthic;
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determine
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                                                                                                                                                                                                                                                                                                                                                   .tis elegans - useful in assaying substances to determin
cell growth, and in inhibiting nematode and insect pests
                                                                                                                                                                                                                                                                                                                                   Potassium channel genes from Drosophila melanogaster and
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94US-0332312.
CYANAMID CO.
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P-PSDB; AAR92315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 42287
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Pred. No. 6.2e-14;
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                       SEQ ID NO 42284
                                                               developmental biology; cell signalling; insecticide;
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                  melanogaster expressed polynucleotide
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Pred. No. 8.2e-14;
0; Mismatches 632;
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 45.4'
Matches 556; Conservative
                                                                                       pharmaceutical; gene; ss.
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                                                                                                                                 Drosophila melanogaster
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P-PSDB; ABB71831.
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ID ABL22074 standard; DNA; 2354
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA, CPD DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                     Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
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Pred. No. 0.53;
0; Mismatches 55,
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 527; 27pp; English.
                                                                                                                                                                                                    Berlin K;
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2000DE-1019173.
2000DE-1032529.
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58.0%;
             15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1043826.
01-SEP-2000; 2000DE-1043826.
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Best Local Similarity 58.0°
Matches 76; Conservative
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                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1318 ttagagtatacttgttatatgttgttttttattaagctgtggaataaaataattattaaaa 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour suppressor gene derived chemically modified sequence #527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 2354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 17695; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2354 BP; 761 A; 460 C; 417 G; 716 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 43.8; DB red. No. 0.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                               Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS46801 standard; DNA; 8237 BP.
                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.2%;
                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 54; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1378 aaaaaaaaa 1388
                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 AGAAAAAAAA 342
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                            WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-2001
                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS46801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ABL34022;

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              Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA innolecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft versus-host disease, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttattgagcacttcgtggacaagccaagtatcttataaaatatttatagcattagagtata 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Designing primers and probes for analysing diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 22; Length 7657;
Pred. No. 1.8;
0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7657 BP; 2028 A; 82 C; 1628 G; 3919 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 182; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL34022 standard; DNA; 7657 BP.
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58.7%;
                                                                                                                                                                                                                                                                   15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-10199173.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1043826.
                                                                                                                                                                                                                                     15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated with cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 58./,
Local 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-602751/68.
                                                                                                                                                                  WO200168911-A2.
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                                                                                                  PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                         olek A,
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                                                                                                                                    Homo
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ID ABL3
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid retweemia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1268 ttattgagcacttcgtggacaagccaagtatcttataaatatttatagcattagagtata 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaenia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                   Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1995; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 24; Length 76
Pred. No. 1.8;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7657 BP; 2028 A; 82 C; 1628 G; 3919 T; 0 other;
                                                                                 immune system associated gene SEQ ID NO: 1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS45389/c
ID AAS45389 standard; DNA; 15732 BP.
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Best Local Similarity 58.7%;
Matches 71; Conservative (
                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                           WO200200928-A2
                                                                                                                                                                                                                                                                            Homo sapiens.
                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                               03-JAN-2002
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                                                                                                                                                                                                                                          gene; ds.
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                                                                                  Human
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Wed Jul

gene therapy; colon cancer; prostate cancer;

SEQ ID NO: 1650

polynucleotide,

(first entry)

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us-08-816-011f-36.rng

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Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                      Human; cytostatic; gene therapy; colon cancer; pr
breast cancer; lung cancer; cancer detection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 780; 1046pp; English.
                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000WO-US18374
                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-091805/10
                                                                                                                                                                                                                                            WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crkenjakov R,
                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams LT,
Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1999;
02-JUL-1999;
                                                                                                  Novel human
                                                         09-APR-2001
                                                                                                                                                                                                                                                                                  11-JAN-2001
                 AAF65894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kita D,
Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinuclectides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis,
                                                                                                                   human immunodeficiency virus; neurodegenerative disorder; solid túmour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds.
                                                         Chemically pretreated complementary DNA associated with cell cycle #47.
                                                                                                    aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                  CpG dinucleotide; cytosine methylation; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15732 BP; 5557 A; 70 C; 2865 G; 7240 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 94; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   ; 20000E-1013847.
; 20000E-1019058.
; 20000E-1019173.
; 20000E-1032529.
; 20000E-1043826.
                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with cell cycle
              18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-602751/68.
                                                                                                  human;
                                                                                                                                                                                                                                                                              WO200168911-A2
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000;
                                                                                                  cycle;
                                                                                                                                                                                                                                                                                                                       20-SEP-2001
                                                                                                                                                                                                    PCR primer
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Kassam A;

Klinger J, Kassam nson G, Drmanac R;

Lamson G,

Innis MA, Garcia PD, Kennedy GC, Pot D, La Dickson M, Labat I, LW, Strache-Crain B;

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Escobedo

C, Randazzo F,

V R, Drmanac S,

Garcia V, Jones

99US-0142310.

Leshkowitiz D;

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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies against them can be used in pharmaceutical compositions to
treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTAGATTAGCTTCTTAGCTGCTCTGTTGATAAACAGAAGACTTTCATTTTCAGGAATG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tattcgaaagaattcatgggatctttgacgattggctcacaacttccaaacgcaagcatt 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 ATCTCCTTCAAAAGTGCCTTAAAGTCAATTTTGGTTGTAATGTATTTGTCTCTGACGTAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGATTCCAACATCTTCCCAAGGCTTTCCCTTCCATAAATTTGTTATAAATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.4; DB 22; Length Pred. No. 1.3; 0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 362 BP; 140 A; 60 C; 87 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 actgaagattccatgtcctggtttttctg 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simil
Matches 103; C
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Indels

Length 15732;

DB 22; 32;

Score 40.8; Di Pred. No. 2.7; 0; Mismatches

2.9%;

Conservative

:09

Best Loca Matches

ò g δ g

Local Similarity

Query Match

1354 tgtggaataaaataattattaaaaaaaaaa 1385

AAF65894/c ID AAF65894 standard; cDNA; 362 BP.

RESULT 10

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The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present interaction of cytosines. The sequences which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, ansemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antianaemic; cytostatic; nootropic; nontanemic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HV; anticonvulsant; ophthalmological; antiinheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18218 BP; 5277 A; 315 C; 3861 G; 8765 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1921; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                     immune system associated gene SEQ ID NO: 1921.
               149 TCTTCAAATTCTCTTTGTTTTTTTTCCTG 121
Berlin K;
                                                                                                           BP
                                                                                                         ABL33948 standard; DNA; 18218
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                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                         gene; ds.
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                                                                                          16938 TAACTAATAAAAAAAAAACTATACTCATAATTTAAAATCTTAACTAACATTTCTAATA 16879
                                                             1303 taaatatttatagcattagagtatacttgttatatgttgtttttattaagctgtggaata 1362
                                  Gaps
 DB 24; Length 18218;
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                                Indels
                                26;
 Score 39.4; Di
Pred. No. 6.6;
                                  Mismatches
                              0;
 2.8%;
67.9%;
                                  Conservative
Query Match
Best Local Similarity
Matches 55; Conserv
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RESULT 12 AAT67765/c

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR mmplification for recombinant polypeptide production, e.g. in E. coli hosts. Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds. Note: This DNA sequence is not reproduced in the specification and has Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter This sequence encodes a H. pylori protein likely to be secreted or H. pylori secreted or periplasmic protein ORF 24256572.aa. Xaa) Xaa) Xaa) Xaa) Xaa) Xaa) been derived from the related specification, WO9719098. aa: Xaa) aa: 881, aa: aa: aa: aa: (pos: 418..420, 6 (pos: 421..423, 6 (pos: 424..426, 6 (pos: 427..429, 6 /transl_except= (pos:
/note= "Xaa = unknown" Mellgaerd BL; :sod) : sod) Location/Qualifiers Claim 23; Page -; 1481pp; English. /transl_except= /transl_except= /transl_except= /transl_except= /transl_except= /transl_except= /transl_except= BP. AAT67765 standard; DNA; 440 96WO-US09122 96US-0630405. (first entry) á 1..440 /*tag= Smith Helicobacter pylori. WPI; 1997-052306/05. P-PSDB; AAW20295 (ASTR) ASTRA Berglindh OT, WO9640893-A1 06-JUN-1996; periplasmic. 07-JUN-1995; 01-APR-1996; 30-JUL-1997 19-DEC-1996 AAT67765;

Gaps ; Length 440; Indels Score 39.2; DB 18; Pred. No. 1.6; 26; 8; Mismatches Query Match 2.8%; Best Local Similarity 51.5%; Matches 68; Conservative E

Sequence 440 BP; 160 A; 68 C; 92 G; 102 T; 18 other;

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Homo sapiens
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Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in
             cttccaagattcactggccgacaccccgttacctcaaatttgccataatcttgcgtgctc 1021
                                                                   ttttcattccattcttcttcttctgcaactatcgtgtccagacgcgtgcttatcctgttt 1081
                                                                                                358 TITICAAGCTCTTTTTTTTTCCTTTTTCCAAATAGCGTTTTTTCATCTCTTACAAATTCTTTGT 299
                                       418 YYACAAAGGCGCGCTGSYYYYYAAAATTTTCCCTCTCTKKTTCTAAAATTTGGCGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence encodes a H. pylori protein likely to be secreted or
                                                                                                                                                                                                                                                                                                                                          Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
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418..420,
421..423,
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a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP;
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                                                                                                                                                                                                                                                                                                                                                        Note: The ORF/protein reference number for this sequence was obtained from the related specification, WO9640893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
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ilarity 51.5%;
Conservative
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06-ARR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1043826.
01-SEP-2000; 2000DE-1043826.
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nes 68; Conservat
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Berlin K;

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Piepenbrock

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Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
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                                                                                                     30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                        The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences:

CSS) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-ollgomentary to (Ss). The nucleic acid may be a peptide nucleic acid-ollgoment (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleide polymorphisms and also to be used in an array for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for accertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters in the diagnosis are disadvantageous to patients. The present sequence is one of the are disadvantageous to patients. The present sequence is one of the analysing cytosine methylations.
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antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; cancer; eye disease; arteriosolerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14112 BP; 2722 A; 568 C; 4223 G; 6599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part
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Claim 1; SEQ ID No 199; 27pp; English.
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Best Local Similarity
Watches 98; Conserv
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reheman, Alzheimer's disease, Alzheitepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1192 tactcaagatttgccgctcagctttccgtttgcactcttatggttggccttctcaccggt 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14112;
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                                                                                                                                                                                                                                                                                                                   Sequence 14112 BP; 2722 A; 568 C; 4223 G; 6599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%; Score 39.2; DB 24;
50.0%; Pred. No. 6.8;
tive 0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1372 ttaaaaaaaaaaaa 1387
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Best Local Similarity 50.0°
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12
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/cgn2_6/ptodata/1/ina/5b_COMB.seq:*
/cgn2_6/ptodata/1/ina/6a_COMB.seq:*
/cgn2_6/ptodata/1/ina/6b_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                          Search time
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US-08-545-196B-10
US-08-545-196B-12
US-08-547-96-1
US-08-553-619B-8
US-08-647-106-2
US-08-464-164-1
US-08-338-057-1
US-08-657-309B-22
US-08-657-309B-22
US-08-993-674A-22
US-08-993-674A-22
US-08-770-379-20
US-08-770-379-20
US-08-770-379-20
US-08-770-379-20
US-08-770-379-20
US-08-781-891-209
US-09-230-371-209
US-09-337-648-7
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                        383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                          nucleic search, using sw model
                                                                                                                                                                                                                                     isting first 45 summaries
                                                          July 23, 2002, 22:11:17
                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                       Issued_Patents_NA:*
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Maximum DB seq length: 2000000000
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32207
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32207
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51259
289
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Match 1
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                                                                                                                              Scoring table:
                                           OM nucleic
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APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
US-08-916-576B-5
US-08-310-165-1
US-09-007-005-32
US-09-007-005-32
US-09-244-796-32
US-09-244-796-3
US-08-621-508-3
US-08-621-33-3
US-08-965-688-3
US-08-965-688-3
US-08-965-688-3
US-09-369-113-3
US-09-369-6118-3
US-09-369-617-3
                                                                                                                                                                                                                                  US-08-213-419B-3
US-09-122-400B-9
US-07-715-751B-2
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3R: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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STATE:
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Sequence Sequence

US-08-742-011-1 US-08-663-112-1 US-09-461-697-1 US-08-415-593-40

US-09-227-357-27

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RESULT 3
US-08-545-196B-12
   US-08-545-196B-10
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                                                                          907 ttgctcacaagtttcctcgtcttcaatttgttcgctgcgattggatccatagttgcttcc 966
                                         Gaps
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APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TILLE OF INVENTION: SURVIVAL MOSCULAR ATROPHY
TITLE OF INVENTION: FOR SPINAL MOSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
   Score 68; DB 1; Length 7218;
Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MELLUM TIRE: ILDM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1267 gttattgagcacttcgtggacaagccaagtatcttataaa 1306
                                       Conservative 234; Mismatches 149;
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08545196B Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
4.98;
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDN
               Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-545-196B-10
   Query Match
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APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS: 65
CORRESPONDENCE ADDRESS:
STREET: PO BOX 747
CITY: FALS CHURCH
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                          Indels
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                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/545,196B
FILING DATE: 19-OCT-1995
Score 38.6; DB 3;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.6; DB 3;
Pred. No. 0.18;
0; Mismatches 34;
                                                                                                                                                                  1356 tggaataaaataattattaaaaaaaaaaaaa 1388
                                                                                                                                                                                       1356 tggaataaaataattattaaaaaaaaaaaaa 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08545196B Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1, 435
CLASSIFCATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: FARACI, C. J. 32,350
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8050
  2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%;
Best Local Similarity 63.4%;
Matches 59; Conservative
Query Match 2.89
Best Local Similarity 63.49
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-08-545-1968-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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1297 atcttataaaatatttatagcattagagtatacttgttatatgttgtttttattaagctgt 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
IP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Slade, Martin B
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 36; DB 2; Length 2621; Best Local Similarity 62.0%; Pred. No. 1.3; Matches 57; Conservative 0; Mismatches 35; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release#10, Version #1.25
SOFTWARE: Patentin Release#10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/55,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATYONEY/AGENT INFORMATION:
NAME: Marcus-Wynner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELEONAMICATION INFORMATION:
TELEPHONE: 415/854.3588
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: NUCLEIC acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric tomato spotted wilt virus S RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORREY/AGBNT INFORMATION:
NAME: Feeney, Joanne Longo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1357 ggaataaaataattattaaaaaaaaaaaaa 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: un
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US-08-553-619B-8
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Pred. No. 0.85;
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               Sequence 1, Application US/08794796

Patent No. 5885800

GENERAL INFORMATION:

APPLICANT: Emery, John

APPLICANT: Trunch, Alem

APPLICANT: Trunch, Alem

APPLICANT: Young, Peter

TITLE OF INVENTION: TR4

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 COMPUTEY: USA
ZIP: 19406
COMFUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 5919705artis Crop Protection STREET: 975 California Avenue CTTY: 910 Alto STATE: CA COUNTY: USA ZIP: 94304 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-553-619B-8
US-08-553-619B-8
Sequence 8, Application US/08553619B
Set part No. 5919705
GENERAL INFORMATION:
APPLICAMT: DeHaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GH50000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA
US-08-794-796-1
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Best Local Similarity
Matches 45; Conserva
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        US-08-794-796-1
                                                                                                                                                                                                                                                                                                                        STATE:
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1318 ttagagtatacttgttatatgttgttttttattaagctgtggaataaaataattattaaaa 1377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bunstead, Janene M.
APPLICANT: Bunstead, Janene M.
APPLICANT: Wermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: EM70-1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Elmeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/338,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5795741
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TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                      TOPOLOGY: 11near MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.69
Best Local Similarity 69.09
Matches 49; Conservative
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          double
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1..1368
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STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
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; LOCATION:
US-08-464-164-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
CLASSIFICATION: 435
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Patent No. 5614195
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Burnstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: S852 base pairs
TYPE: NOTLEIC ACID
STRANDEDNESS: Single
TOPPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INPOMATION:
NAME: Gormley, Mary E.
REGISSRATION UNDMER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                     CDS
2378..5038
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2378..5038
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LOCATION:
FEATURE:
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; LOCATION:
US-07-867-106-2
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                                                                                                                                                                                                                          FEATURE
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PREVENTION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
CORRESPONDENCE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                 Length 1400;
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                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                         LIBRARY: sporozoite cDNA cloned in Lambda ZAPII CLONE: Em70-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                               Score 35.8; Di
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08557309B Patent No. 5916572 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 DEVELOPMENTAL STAGE: sporozoite IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%;
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                                                              Eimeria maxima
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                          C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 581 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                      1..1368
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Best Local Similarity
                                                                                   STRAIN: Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                        FRAGMENT TYPE: ORIGINAL SOURCE:
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US-08-557-309B-22
                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-668-416-1
                                                            ORGANISM:
        ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                  Score 35.8; DB 1; Length 1400;
Pred. No. 1.1;
0; Mismatches 22; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08668416
Patent No. 5843722
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bunstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5843722el Patent Department
                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Akzo No. 5843722el Patent Department
1300 Piccard Drive, Suite 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/668,416
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
ATTORNEY AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
                                                                                                                 STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%;
Best Local Similarity 69.0%;
Matches 49; Conservative C
MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                 Eimeria maxima
                                                            C-terminal
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                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..1368
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                                        ANTI-SENSE: NO
FRAGMENT TYPE: C-
ORIGINAL SOURCE:
ORGANISM: Eimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20850
                                                                                                                                                                                                                                                       ; LOCATION:
US-08-338-057-1
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PREVENTION OF

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1296 tatcttataaatatttatagocattagagtatacttgttatatgttgttttttattaagctg 1355
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: McMell, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 81
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                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
CLEASIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.422C2
REFERENCE/DOCKET NUMBER: 210121.422C2
TELECOMMUNICATION INFORMATION:
TELEFAM: (206) 682-6930
TELEFAM: (206) 682-6931
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANOLA TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN TITLE OF INVENTION: THE REGULATION OF FATTY ACID TITLE OF INVENTION: CONTENT OF THE OILS OF SOYBEAN TITLE OF INVENTION: AND CANOLA PLANTS

NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
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                                                                                                                                                               3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.4; DB
Pred. No. 0.89;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1356 tggaataaaataattattaaaaaaaaaaaaaa 1388
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                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HITZ, WILLIAM DEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.6%;
Best Local_Similarity 61.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Conservative
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU
STREET: 1007 MARKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM
                                                                                                                                                                                   STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: HITZ, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: DELAWARE
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US-08-793-410-11/c
                                                                                                                                                               ADDRESSEE:
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                                        1296 tatcttataaaatatttataggattagagtatacttgttatatgttgttttttattaaggtg 1355
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Sketky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: HOUGHON: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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Pred. No. 0.89;
0; Mismatches 36; Indels
  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
CLASSIFICATION: 424
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6300 Columbia Center, 701 Fifth Avenue
  Mismatches
                                                                                                                       1356 tggaataaaataattattaaaaaaaaaaaaaa 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08993674A Patent No. 6228372 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                            US-08-834-306-22; Sequence 22, Application US/08834306; Patent No. 6054135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.6%;
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Best Local Similarity 61.39
Matches 57; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Washington
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDALL
STREET: 6500
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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57;
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Matches
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1282 CCTCCTCGTCCTTCTTGTCCTCCTCCTCGTCCTCCTCGTCCTCATTGTCCTCAT 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: White, John P.
RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                     2.6%; Score 35.4; DB 2; I
57.8%; Pred. No. 2.2;
tive 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AEDRI INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 32207 base pairs TYPE: nucleic acid
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Best Local Similarity 57.84
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                               US-08-728-323A-1
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                                                                                                                                                                                                                                                                         FEATURE
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APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Bohenzky. Roy A.
APPLICANT: Redelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.4; DB
Pred. No. 1.3;
0; Mismatches
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MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE OPPERATING SYSTEM: MICROSOFT WINDOWS 95 SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION NUMBER: US/08/793,410
                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TLING DATE: AUGUST 25, 1995
ATTORNEY AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: 30,971
RELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEPHONE: 302-992-5481
TELEPHONE: 302-973-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08728323A
Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6%;
Best Local Similarity 61.3%;
Matches 57; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-728-323A-1/C
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Gaps

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Indels

Length 3489;

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match

Query Match

Ast Local Similarity 57.84; Pred. No. 6.8;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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